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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                     NO
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                               Score
                   194.8
107.6
98
93.2
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Match Length
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2: \(\silbs2\)gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
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5: \(\silbs2\)gcgdata/geneseq/geneseqn-embl/NA1985.DAT: *
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7: \(\silbs2\)gcgdata/geneseq/geneseqn-embl/NA20001.DAT: *
7: \(\silbs2\)gcgdata/geneseq/geneseqn-embl/NA2001.DAT: *
7: \(\silbs2\)gcgdata/geneseq/geneseqn-embl/NA20002.DAT: *
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Rose 1-aminocyclop
Arabidopsis thalia
Broccoli ACC synth
DNA encoding a 1-a
1-aminocyclopropan
1-aminocyclopropan
ACC synthase GAC-2
Pelargonium 1-amin
Broccoli ACC synth
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Key CDS misc misc misc misc misc	N30330 AAV30330 AAV30330 AAV30330 AAV20330 28-SEP-19 Rose 1-an ACC syntl ethylene; Rosa sp.	44444433333333300000000000000000000000
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	0 standard; cDNA; 17 0; 1998 (first entry) aminocyclopropane-1- thase; 1-aminocyclop e; transgenic plant; . cv. Cardinal Red.	220 200 200 200 200 200 200 200 200 200
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leotide (Claim 18)" leotide (Claim 18)" leotide (Claim 18)"	hase cDNA pRoseKacc7. late synthase; pRoseKacc7; ss.	Poplar 1-aminocycl Mangifera indica A CC Synt Carnation ACC synt Carnation ACC synt Carnation ACC synthatease gen ACC synthatease GAC-1 Clone pACC1 encodi Zucchini ACC synth Zucchini 1-aminocy Zucchini 1-aminocycl Tomato ACC synth Mung bean ACC synth Mung bean ACC synth Carica papaya ACC Clone ptACC1 encod Tomato 1-aminocycl Tomato ACC synthas Tomato 1-aminocycl Tomato ACC synthas Crucifer 1-aminocycl Toma insert of 13 T-DNA insert of 13 ACC synthase Carica papaya ACC Zucchini ACC Synthas Carica papaya ACC Zucchini ACC Synthas Carica papaya ACC Zucchini ACC Synthas

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                                                                                                                                                          Matches
                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated ACC synthase genes - a rose, used to develop products for ethylene levels, for increasing she
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                                                                                                   TTCCAGGTTTCAGGGTGGGTGCCATCTACTCCTTTAACAAGAATGTCTTGACTGCTGCTA
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complement (351..400)
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71.2%;
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ment (251..300)
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                                                                                                                                                         Score 194.8; DB 19;
Pred. No. 9.8e-58;
0; Mismatches 112;

    are obtained from geranium and
for producing plants with reduced
shelf-life

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(ANYY/)
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Rameaka JG,
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(SLAT/)
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MATHEW A V.
LEDFORD B L.
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SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
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GARCIA C A.
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Ledford BL,
C, Davis KR,
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BL, Woessner
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Hoffman
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man N;
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useful e.g. for preparing transgenic or altered metabolism – $\,$

New nucleic acid that hybridizes to Arabidopsis thaliana sequences.

plants with increased resistance

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RESULT 3
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ID AAT3
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                                       exor
                                                                                                                                                                                                                                                           antisense; broccoli;
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                                                                                                                                              location/Qualifiers
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea genomic clone ACCAl (AAT33136) codes for 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase) (AAR98598), an enzyme involved in ethylene biosynthesis. It was obtd. by subjecting broccoli leaf total genomic DNA to PCR using primers (see also AAT33137-38) based on the Arabidopsis thaliana ACS ynthase gene. The product was cloned into PCRII to obtain clone ACCAl. Genomic DNA or cNAM (see also AAT33139) can be inserted, in sense or antisense orientation, into an expression cassette and the transferred to a binary vector suitable for Agrobacterium-mediated plant transformation. The constructs permit control of the level cacc synthase in a transgenic plant (esp. B. oleracea or Cucumis melo) and hence a control of maturation, ageing and shelf-life.
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                                                                                                                                                                1030
                                                                                                                                                                                                                                                                                                                           Sequence 1384 BP; 401 A; 290 C; 310 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Fig1A-B; 50pp; English.
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in plants, esp. to improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of Brassica oleracea - used to regulate ethylene-dependent processes in plants, esp. to improve shelf life
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P-PSDB; AAR98598.
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TAATGCAGGGT--TGTTCTGTTGGATGAATTTGGGTTTCTTGCTCGACACGAAAACGAAA
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                                                   AGACGGTACGAGACAATTGTGGAAGGGCTT-AAGAAGGCAGGGATCGAGTGTTTGAAGGG
                                                                                AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
                                                                                                         ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG 1149
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1352..1382
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135.431
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432..594
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595..1384
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Pred. No. 1.1e-23;
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                                                                                                                                                                                                                                                                                                                           383 T; 0 other;
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                                                                                                                                                                                                                                                                                               Length 1384;
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RESULT 4
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AC AAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes methods for introducing localized mutations into target genes in plant cells. The methods comprise using a recombinogenic oligonucleobase comprising 2 regions homologous to a target gene and an intervening mutant region. The methods can be used to introduce localized mutations into target genes to introduce desirable traits, e.g. selective growth advantage under appropriate selective conditions, change in colour of plant cells growing in a callus, herbicide resistance, or improved preservation of fruit or flowers. They can be used in plants such as maize, wheat, rice, lettuce, potato, tomato, canola, soybean or cotton cell. The present sequenc represents
                                                                                                                                                                                            2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Introducing mutations into target genes in plant cells recombinogenic oligonucleobase comprising 2 regions hor target gene and an intervening mutant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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herbicide resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       target
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ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                                                                                                                                                                       GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
                                                                                   GCTACAAAATGTCAAGTTTCGGCCTTGTCTCCTCCCAGACACAATACCTACTATCCTCA
                                                                                                                                                                                            GCCTCCCTGGTTTTAGAGTTGGAGCCATTTACTCCAATGACAAAGATGTCATCTCTGCC 2353
                                                                                                                                   GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   3438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the methods of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                BP; 1084 A; 647 C; 599 G; 1108 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tion; target gene; plant cell;
oligonucleobase; selective growth advantage;
stance; preservation; fruit; flower; ss.
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                                                                                                                                                                                                                                                                                                                                Score 93.2; DB 20 Pred. No. 8.3e-22;
                                                                                                                                                                                                                                                                                                      Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        мау
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                                                                                                                                                                                                                                                                                                                                                                3438;
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(QUEE-)
(UYQU )
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                                                                                                                                                             01-MAY-1996;
                                                                                                                                                                                                06-NOV-1997
                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                               Ananas
                                                                                                                                                                                                                                                                                                                                                                                                flowering;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV00220 standard; DNA; 961
                 Claim 2;
                                     is inhibited
                                              New isolated ACC synthase genes from pineapples – used transgenic pineapples in which the natural initiation of
                                                                          P-PSDB;
                                                                                  WPI; 1998-009279/02
                                                                                                    Botella J, Sanewski G;
                                                                                                                                                                               01-MAY-1997;
                                                                                                                                                                                                                   AU9719963-A.
                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                 1-aminocyclopropane-1-carboxylic acid; ACC synthase;
flowering; inhibition; regulation; development; frui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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                                                                                                                      GOLDEN CIRCLE LTD STATE QUEENSLAND. UNIV QUEENSLAND.
                                                                          AAW37445
                Fig
                                             pineapples
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                 2; 37pp;
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                                                                                                                                                                               97AU-0019963
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194..961
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102..193
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                                                                                                                                                                                                                                                                                                                                  /product=
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                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                  English
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                                               of flowering
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The present sequence represents

the nucleotide sequence encoding

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RESULT 6
AAVO219
ID AAVO
XX AAVO
AC AAVO
DT 08-J
XX 1-am
XX 1-am
XX 1-am
XX 1-am
XX ADAN
EFT CDS
FT CDS
FT CDS
FT XX AD97
PN AU97
PN AU97
PF 01-b
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Matches
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   01-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of pineapple. The present invention describes a transgenic variety of pineapple in which initiation of flowering is inhibited, the variety comprising a nucleotide sequence encoding an ACC synthase enzyme where the nucleotide sequence is operably linked, in the sense or antisense orientation, to one or more regulatory nucleotide sequences. The ACC synthase gene can be used to regulate pineapple plant development,
                               06-NOV-1997.
                                                              AU9719963-A.
                                                                                                                                                                                                                                     l-aminocyclopropane-1-carboxylic acid; ACC synthase; pineapple;
flowering; inhibition; regulation; development; fruit; ss.
                                                                                                                                                                                                                                                                                  1-aminocyclopropane-1-carboxylic acid
                                                                                                                                                                                                                                                                                                                     08-JUN-1998
                                                                                                                                                                                                       Ananas comosus
                                                                                                                                                                                                                                                                                                                                                                                   AAV00219 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly for inhibiting initiation of flowering. Such plants can then be induced to flower in a narrow spectrum of time which would thereby decrease the spread of fruit maturity within a crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 924
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hes 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTCTT 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAATGCAGGGT - - TGTTTTGGTTGGGTGGACATGAGGCACTTACTTAAGTCTAAGACACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGCGGCAAAAGCGGCTCACCGAAGCGCTGCGGACGATCGGTATAAACTGTTTGGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          961 BP;
                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 930
 97AU-0019963
                                                                                         /transl_except= (pos:967..968,aa:Val)
/note= "no stop codon given"
                                                                                                                           /product= "acacc2"
                                                                                                                                                                          Location/Qualifiers
                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 A;
                                                                                                                                                            . . 968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 C;
                                                                                                                                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86.6; DB 19;
Pred. No. 9.2e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 159;
                                                                                                                                                                                                                                    development; fruit;
                                                                                                                                                                                                                                                                                  synthase gene acacc2
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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the nucleotide sequence is operably linked, in the sense or antisense orientation, to one or more regulatory nucleotide sequences. The ACC synthase gene can be used to regulate pineapple plant development, particularly for inhibiting initiation of flowering. Such plants can then be induced to flower in a narrow spectrum of time which would thereby decrease the spread of fruit maturity within a crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GOLD-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the nucleotide sequence encoding a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase enzyme of pineapple. The present invention describes a transgenic variety of pineapple in which initiation of flowering is inhibited, the variety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated ACC synthase genes from pineapples - used to generate transgenic pineapples in which the natural initiation of flowering is inhibited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            comprising a nucleotide sequence encoding an ACC synthase enzyme where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1996;
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les 208;
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                                                                                                                                                                                     GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTT
                                                                                                                                                                                                                                                  AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC
                                                                                                                                                                                                                                                                                                               GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTT 120
                                                                                                                                                         GGATCTTCATGCCACTGCTCTGAGCCTGGCTGGTT
                                                                                                                                                                                                                      GAAGGGGAGCTCAGCCTGTGGAAACTGATATTGCATGAGGTGAGGCTCAACATATCACCA
                                                                                                                                                                                                                                                                                   AATGCCGGGCTGTTC---TGCTGGATGAATCTGGGGCCACTCCTCGAGGAGCAGACGAGA
                                                                                                                                                                                                                                                                                                                                              AGGAGGTACGAGTACATAATCCAGGGGCTGGAGAGAGCAGGGATTGAGTGCTTCCAAGGG
                                                                                                                                                                                                                                                                                                                                                                    AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                             ATGCTGTCGGACGAGGAGTTCACAAAGTACTACATAAGGACCAACAGGGAGAGGCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  968 BP; 241 A; 235 C; 294 G; 198 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanewski G;
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Pred. No. 4.7e-19;
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28-JUL-1997 AAT66247

(first entry)

AAT66247 standard;

DNA;

1170

ВP

ACC

synthase GAC-2

DNA

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; antisense; ethylene; transgenic plant; Pelargonium x domesticum; in vitro propagation; tissue culture; ripening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Commercial propagation especially Pelargonium
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                                                                                                                                  1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
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                                                                      AAAGGAGAGCTOGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC
                                                                                                                                                                            AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                          GCGCGAAAGATGTCAAGTTTCGGCCTTGTATCCACACAAACTCAGCACCTAATCGCATCA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTTCCCTGGCTTCAGGGTGGGGATTGTCTACTCCTACAATGACGCAGTTGTGAATTGT
GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                          GAGGCGGAGATGGCTCTGTGGAGAGTGATAATCAATGAGGTGAAGCTAAATGTGTCGCCA 1119
                                                                                                                                  CAATGGGGGGTTATTCAT - - ATGGATGGACTTGAGGAGGGCTTCTCAAGGAGAAGACTTTC
                                                                                                                                                                                                                           AGAAGGTACGCAACCTTCACAAGAGGGCTTGCA-CAAGTCCACATTGGGAGCCTAAAGAG
                                                                                                                                                                                                                                                                                                                    ATGCTCTCGGACGATGAATTCGTGGACACATTCATCGTGGAGAGCGCGAAGAGGCTAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTC
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217; Conser
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ilarity 53.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83.6; D: Pred. No. 1.2e 0; Mismatches
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1.2e-18;
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RRESULT 8
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                      P-PSDB; AAW60235
                                             WPI; 1998-260994/23
                                                                                      Ranu RS;
                                                                                                                                                                          01-OCT-1996;
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ylene; transgenic plant; wilting; geranium; pPHSacc49;
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complement (101..150)
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complement (1..1878)
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complement (351..400)
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complement (301..350)
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complement (451..500)
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                                                                                                                                                                                                                                                                                                     1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1192
                 antisense; broccoli; ss
                               ACC synthase; 1-aminocyclopropyl-1-carboxylic acid synthase; ethylene; shelf-life; Cucumis melo; melon; transgenic plant;
                                                                                          Broccoli ACC
                                                                                                                               07-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced ethylene levels, for increasing shelf-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yellowing and petal abscission during shipping and storage.
                                                                                                                                                                                                                                                                                                                                        361
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                                                                                                                                                                                                                                                                                                                        GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG
                                                                                                                                                                                                                                                                                                                                                                         GAGGCGGAGATGGCTCTGTGGAGAGTGATAATCAATGAAGTGAAGCTAAATGTGTCGCCA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA clone, designated pPH5acc49 (ATCC 98179), codes for a kDa 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) AAW60235) of geranium (Pelargonium x hortorum cv. Sincerity).
                                                                                                                                                                                                                                                                                                   GGGGCGTCGTTCCATTGCTCGGAGCCAGGGTGGTTTAGAGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAACTCGGCATCCGATGCACGGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                               AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATGGGGGGTTATTCAT--ATGGATGGACTTGAGGAGGCTTCTCAAGGAGAAGACTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCGAAAGATGTCAAGTTTCGGCCTTGTATCCACACAAACTCAGCACCTAATCGCATCA 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clone, designated pPHSacc49 (ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
217; Conserv
                                                                                                                                                                                                    standard; cDNA;
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                                                                                        synthase cDNA clone TA13.
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53.7%;
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Pred. No. 1.5e-18;
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Matches 203
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ACC synthage in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA. The PCR product was cloned into pCRII to obtain clone TA31. cDNA or genomic DNA (see also AAT33136) can be inserted, in sense or antisense orientation, into an expression cassette and the transferred to a binary vector suitable for Agrobacterium-mediated than the construction of the level of the l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea cDNA clone TA13 (AAT33137) codes for 1-aminocyclopropyl-1-carboxylic acid synthase (ACC-synthase) (AAR98599), an enzyme involved in ethylene biosynthesis. It was (AAR98599) are enzyme involved in ethylene biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding 1-amino:cyclo:propyl-1-carboxylic acid synthase of Brassica oleracea - used to regulate ethylene-dependent processes in plants, esp. to improve shelf life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nt transformation. The constructs permit control of the level synthase in a transgenic plant (esp. B. oleracea or Cucumis o) and hence a control of maturation, ageing and shelf-life.
                         AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC
                                                                                                                     ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                   GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                       TAATGCAGGGT - - TGTTCTGTTGGATGAATTTGGGTTTCTTGCTCGACACGAAAACGAAA
                                                                                                                                                                                                                      AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
                                                                                                                                                                                                                                                                    ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG
                                                                                                                                                                                                                                                                                                                                                                     GGTCTTCCCGGTTTTCGAGTTGGGACCATTTACTCGTACAACGATAATGTTGTGAGGACA
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                                                                                                                                                                     AGACGGTACGAGACAATTGTGGAAGGGCTT-AAGAAGGCAGGGATCGAGTGTTTGAAGGG
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/note= "primer F
975..993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%;
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Pred. No. 3.3e
0; Mismatches
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                                                                                                                                                                                             Matches
                                                                                                                                                                                                       Query Match
Best Local
                                                                                  1004
                                                                                                                                                                                                                                                                                                                                                                                                                        Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic enzyme genes - from poplar tree, are useful for generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                            1064
                                                                                                                                                                                                                                                Sequence 1868
                                                                                                                                                                                                                                                                                   This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase gene isolated from poplar trees whice had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone for 6 hours after one hour acclimation at 25 degrees C, 70 % relationality, 30 k lux and air current 30 cm/second. This gene will be useful for breeding air pollutant ozone-resistant trees, especially
                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                            ozone-resistant trees and pollution clean-up trees
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW21755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-239270/22.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-1995;
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es 216; Conserv
                                                                                                           GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT
                                                                                                                                       GGACTCCCTGGCTTCAGAGTTGGAATTGTTTACTCATACAACGATGCAGTTGTTAATTGC 1003
                                                                                                                                                     GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCTTCGT 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTCTTGT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGGCGAGCTCGAGCTTTTGGGTGTGATCTTGAAGGAACTAAAGCTGAATATATCTCCT 977
 AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
                                                     ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                  GGCCGAAAGATGTCAAGTTTTGGTCTGGTCTCCTCACAAACTCAATATTTACTTGCTTCA 1063
                            ATGCTTTCTGATGAAGAGTTTGTCGAGGATTTCCTAGCCGAGAGCTCGAAGAGGCTAAAG
                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                  Pages 9-11; 12pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                BP; 590 A; 366 C; 405 G;
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                                                                                                                                                                                          Score 82; DB 18;
Pred. No. 5.4e-18;
0; Mismatches 185
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                                                                                                                                                                                                                                                507 T; 0 other;
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                                                                                                                                                                                            185;
                                                                                                                                                                                                                     Length 1868;
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AAT73501
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                                                                                                      Matches
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Best Local S
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     1025
                                                                                                                                                                                                                                                                             This sequence, designated PNACCS1, is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase gene isolated from poplar trees which had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone for 6 hours after one hour acclimation at 25 degrees C. 70 % relative humidity, 30 k lux and air current 30 cm/second. This gene will be useful for breeding air pollutant ozone-resistant trees, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic enzyme genes - from poplar tree, are useful for generating ozone-resistant trees and pollution clean-up trees
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Pages
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT73501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT73501
                                                                                                                                                                                                       Sequence 1864 BP; 574 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TOYT ) TOYOTA JIDOSHA KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ozone; induction; exposure; resistance; 1-aminocyclopropane-1-carboxylic acid b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS1
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                                                                                                                                                                                                                                                        poplar.
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                                                                                                      Local Si
hes 202;
1997-239270/22
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                                                                                                                             Similarity
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                                                                                                        Conservative
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                                                                                                                                                                                                         360 C;
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                                                                                                      Score 80.8; DB 18;
Pred. No. 1.4e-17;
0; Mismatches 202;
                                                                                                                                                                                                         392 G; 538 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1864
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biosynthesis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                     ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; miaccl; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1385
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This sequence represents a novel gene, miaccl,
                       Claim 4; Fig 4; 46pp;
                                             Pineapple, papaya and mango ACC synthase genes - therapy to produce fruits with reduced senescence
                                                                                  WPI; 1997-202875/18.
P-PSDB; AAW18289.
                                                                                                                                                                    02-MAY-1996;
20-SEP-1995;
                                                                                                                                                                                                                                                      WO9711166-A1
                                                                                                                                                                                                                                                                                                                                                                                   Mangifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mangifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT72631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT72631 standard;
                                                                                                                    Botella
                                                                                                                                         (UYQU ) UNIV
                                                                                                                                                                                                      20-SEP-1996;
                                                                                                                                                                                                                              27-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
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                                                                                                                                                                                                                                                                                                                                                                                                         4.4.1.14; mango; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCTCTCGGACACGCGGTICACTCAAAAGTTCATCGAGGTAAACAGAGCGGAAACTCAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTGCTCTTTCATTGCTTGAAGCCAGGGTGGTTTAGGGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCGCAAGATGTCAAGCTTCGGATTGGTATCCACAAACTCAGTACCTGATAGCATCA 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                                                                    JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indica ACC synthase miaccl gene
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                                                                                                                                            QUEENSLAND
                                                                                                                                                                 96AU-0009603.
95AU-0005559.
                                                                                                                                                                                                      96WO-AU00591;
                                                                                                                                                                                                                                                                                     /product= miacc1
/EC_number= 4.4.1.14
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                                                                                                                                                                                                                                                                                                                                                   1..1096
                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                        English.
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RESULT 13
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of an ACC synthase multigene family found in mango. ACC synthase is involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control
                                                                                                                                                                                                                          ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; miacc2; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1045
WO9711166-A1
                                                                                                                                                                              Mangifera indica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1096 BP; 302 A; 227 C; 255 G; 312 T; 0 other;
                                                                                                                                                                                                             EC 4.4.1.14; mango; multigene family;
                                                                                                                                                                                                                                                                                                 Mangifera indica ACC
                                                                                                                                                                                                                                                                                                                                 27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                   AAT72632 standard; DNA; 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reducing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTCTTCCTTTCATTGCCAGGAGCCTGGTTGGTTCAGAGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGCCGAAATGAAGCTATGGGGGCACGATTTTGAACGATGTGAAACTTAACGTTTCACCA 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATGCAGG--TCTTTTCTTCTGGATGGATTTGCGACACCTCCTTCAACAAGAAACAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                (first entry)
                                                              /EC_number= 4.4.1.14
/product= miacc2
/note= "Sequence rep
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1..1113
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                                              "Sequence represents 75% of the coding sequence and does not contain the sta
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                               or stop codons
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Pred. No. 1.5e
0; Mismatches
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1.5e-17;
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                                                                RESULT 14
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the novel gene, miacc2, which is a member of the mango ACC synthase multigene family. ACC synthase an enzyme involved in the pathway for ethylene biosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene is often deleterious to crops, especially if some form of mechanical wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senescence and thus improving storage life.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pineapple,
therapy to
           AAX27501;
                                                                                                         1051
                                      AAX27501 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
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20-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT
                                                                                                                         GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG
                                                                                                                                                            GAAGCAGAGATAGAACTGTGGAAAGTGATAATCAACGAAGTTAAATTAAATGTTTCTCCG
                                                                                                                                                                                       AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC 360
                                                                                                                                                                                                                                                                                    AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAACTCGGCATCCGATGCACGGAAAG
                                                                                                         GGTTCTTCCTTTCATTGCGCTAATCCAGGATGGTTTCGGGTTTG
                                                                                                                                                                                                                CAATGCGGG--GCTATTTTCTGGATGGATTTGCATCATCTCCTCAAGGAGCAAACTGAT
                                                                                                                                                                                                                                                                     AAAAGGCACAGAGCCTTC-ACATGGGGGCTATCTCAAGTAGGCATTGGTTGTTTGAAGAG
                                                                                                                                                                                                                                                                                                                          ATGTTATCAGATGAAGTTTGTGGATAGGTTCATTACTGAGAGTGCTAAAAGGCTTGCA 873
                                                                                                                                                                                                                                                                                                                                                                              GCCTGCAAAATGTCAAGCTTTGGACTTGTATCATCACAAACTCAACATTTAATCGCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al Similarity
215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           papaya and mango ACC synthase produce fruits with reduced se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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95AU-0005559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 A; 212 C;
                                      cdna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.9%;
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                                      1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 1.5e
0; Mismatches
                                      ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
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                                                                                                                                 404
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                                               Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                        (pacos7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (acs) (c) and an ethylene forming enzyme (EFE), respectively. The clones are deposited under the Accession Numbers NCIMB 40813 and NCIMB 40814, cc respectively pasc6 and pacos7 may be used to genetically control cc processes involved in fruit ripening (and other ethylene related cc processes). Vectors comprising the cDNA sequences may be used to produce crosses). Vectors comprising the cDNA sequences may be used to produce constructs and pacos7 used in the construct, will determine construct, will determine constructs, and transcribe mRNA that encodes an active enzyme, the rate constructs can also be used to up-regulation) (however, full-length sense constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to intension and the enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can also be used to inthe enzyme expression by constructs can express encode antisense mRNA, they will inhibit the constructs of the genes involved in fruit ripening and hence slow the process down (down regulation). In this manner different spatial and fine temporal pattalling the constructs of the constructs of
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         temporal patterns of genes expression can be produced. Retardation rate of ribening will reduce the rate of deterioration of banana fi after harvest. This helps in production of high quality fruit that improved flavour and texture. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated cDNA molecules ((pASC6) and (pACOS7)) encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS) and an eforming enzyme (EFE) - useful for modifying fruit ripening characteristics, especially in bananas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Musa
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-228611/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5886164-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-aminocyclopropane-1-carboxylic acid synthase; A ethylene forming enzyme; ethylene biosynthesis; p transgenic; enzyme; inhibition; flavour; texture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZENE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transgenic;
                                                                                                                                                                                                                                              865
                                                                                                                                                                                                                                                                                                                                        Local Sim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                           GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT
                                                                                                                                                                        AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
                                                                                                                                                                                                                                           GGCGTCCCTGGCTTCCGCGTCGGCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924
                                               ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 104
                                                                                            ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                                                                               GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-aminocyclopropane-1-carboxylic
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        1712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the banana ACS enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Columns 11-14; 22pp; English
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to two isolated cDNA molecules ((pASC6) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0632598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0632598
                                                                                                                                                                                                                                                                                                                                                                                                                                        397 A; 459 C; 478 G; 378 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                               19.5%;
53.0%;
                                                                                                                                                                                                                                                                                                                                        Score 78.8; DE Pred. No. 6.9e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                               DB 20;
.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid
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plant; fruit ripening;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                       The sequence represents the coding sequence of 1-aminocyclopropane-1-
CC carboxylic acid synthase (ACS) from banana, used in the method of
CC the invention. The method involves modifying the level of ethylene
CC biosynthesis in a plant of the genus Musa by inserting into the genome of
CC the plant a DNA sequence (1) encoding a banana 1-aminocyclopropane-1
CC carboxylic acid synthase (ACS) or an ethylene-forming enzyme (EFE), where
CC (1) is in sense or antisense configuration, and modifies the level of
CC activity of ACS or EFE. This retards the rate of ripening in banana
CC fruits which reduces the rate of deterioration of banana fruit after
CC harvest. As a result, fruit may be harvested when they have reached
CC partial or full ripeness and still have the robustness to withstand
CC handling and transport to reach the consumer in good condition. In this
CC way high quality ripe fruit can be made available to the consumer with
CC reduced requirement for post-harvest treatment. High quality fruit will
CC have improved flavour and texture. High quality fruit can be produced
CC consistently over a wide harvest period, and such fruit can be held in
CC store for long periods and ripened to optimal quality by the supply of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modifying level of ethylene biosynthesis in plant of genus Musa, involves inserting into genome of plant a DNA sequence encoding banana 1-aminocyclopropane-1-carboxylic acid synthase or ethylene-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Column 13; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-450497/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Musa sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-aminocyclopropane-1-carboxylic acid synthase; ACS; ethylene biosynthesis; ethylene-forming enzyme; EFE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding 1-aminocyclopropane-1-carboxylic acid synthase (ACS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
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                                                                    ethylene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fletcher JD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  banana;
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Best Local Similarity
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                          GAGGCGGACGTCCGGCTGTGGCGGGTGATCATCAACGACGTGAAGCTCAACATCTCGCCG 122
                                                       AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
                                                                                    GGGCGGCGCAGGGTCTTTACGG-ACGGCCTCAAGCGAGTCGGGATTCATTGCTTGGACGG 1103
                                                                                                                                                                          AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
                                                                                                                                                                                                                                     ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                                                                                                                                                                                                    GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC 984
                                                                                                                                                                                                                                                                                                 GGCGTCCCTGGCTTCCGCGTCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924
GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG
                                                                                                                                                                                                         ATGTTGGGAGACGAGGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 1044
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 78.8; DB 22;
Pred. No. 6.9e-17;
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Search completed: March 11, Job time: 181 secs 2003, 00:52:07

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Copyright (c) 1993
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
AF184076
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VERSION REFERENCE SOURCE ORGANISM KEYWORDS AUTHORS TITLE $\begin{array}{ll} {\tt Mbeguie-A-Mbeguie,D.} & {\tt and Fils-Lycaon,B.R.} \\ {\tt Molecular cloning and nucleotide sequence} \end{array}$ Spermatophyta; Magnoliophyta; eudicotylorsidae; eurosids I; Rosales; Rosaceae; 1 (bases 1 to 894) Prunus armeniaca AF184076 AF184076.1 GI:10 Prunus armeniaca Eukaryota; Viridiplantae; Prunus AF184076 armeniaca. GI:10441264 ACC synthase Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; 894 bp bp DNA (ACS1) ge gene, Amygdaloideae; of genomic DNA encoding linear PLI partial cds PLN 01-0CT-2000

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Vegetaux, Institut National de la Recherche Agronomique,
Agroparc-Domaine Saint Paul, Avignon 84914, France
                       gene, par
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RFSSISTPSQQLLSSMLSDTKFVQKFIDANRERLRGMHLKFLTGLKQLGIETKSNGG
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/gene="ACS1"
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    Arabidopsis thaliana 1-0 ACS10 (At1g62960) mRNA, AF348575
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TGTCACTGTATTGAACCTGG
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                                         TGTCATTGTATTGAACCCGG
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1 (bases 1 to 581)

Xu,C., Chen,K., Chen,D. and Zhang,S.

Molecular cloning of four members of ACC synthase gen kiwifruit (Actinidia chinensis Planch.)
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People's Republic of China
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1112 c 132 g 171 t
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Pred. No. 9e-46;
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thaliana 1-aminocyclopropane-1-carboxylate 62960) mRNA, complete cds.

1674 bp

mRNA

linear

PLN 18-APR-2002

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                                                                                                     CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
                                                                                                                                                                                                                                      TTCCGGGGGCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 1251
                                                                                                                                                                                                                                                                               TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 63
ATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243
                                                                 ATCTCCAATCCAAAAAATGTTCAGAGATTTGTGAAAACCAACAGGCAGAGATTGCAGAGT 1371
                                                                                                                                                   AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 1311
                                                                                                                                                                                           ANANAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-FEB-2001) Plant Gene Expression Center, Street, Albany, CA 94710, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada,K., Liu,S.x., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., BrocChao,Q., Chen,H., Cheuk,R., Karlin-Neumann,G., Kim,C., Lam,B. Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
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Spermatophyta; Macnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                          Conservative
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AGHLTELTGLPRSLSRILLSPRNSGGAVSVSGRVNCVLKGGDSSPYTVGQKRVEDDPY
DELGNPDGYIQLGLAQNNKLSLDDWYLENPKEAISDGLSISGIASYEPSDGLILELKMA
VAGFMTEATKNSYTFDPSQLYLITSGASSAIELLSFCLADSGNAFLVPTPCSPGYDRDV
KWRTGVDLIHVPCRSADNENMSMVYLDRAFYQAKKRGVRIRGIIISNPSNPMGSILLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKINVIPGSCCHCIEPGWFRICFSNLSERDVPVVMNRIRKVCETCKSQN"
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SKDLSFRGLRSAAIYSFNESVLSASRKLTTLSPVSSPTOHLLISAISNPKNVQRFVKT
NRQRLQSIYTELVEGLKELGIECTRSNGGFYCMADMRGLISSYSEKGEIDLWNKLLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAK15546.1"
/db_xref:"GI:13194768"
/translation="MTRTEPNRSRSSNSDSDKNSGNVGGGRTTGMRVIVPLQGVVQGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="This clone is ecotype: Columbia"
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/product="1-aminocyclopropane-1-carboxylate synthase
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/db_xref="taxon:3702"
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Pred. No. 5.2e-36;
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AY054691 11555
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                                                                                                                                                                                                                                                                                                                                                                                                               Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out sequencing and annotation of the RaFL cDNAS: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C. Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collection and clustering of RAFL cDNAS (RAFL CDNA: ''RIKEN Arabidopsis Full-Length cDNA''): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genomic Sciences Center (GSC) members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada, K., Ecker, J., Theologis, A. and
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/product="Strong similarity to ACS5 from Lupinus albus gb|AFI19414, and contains an Aminotransferase-classI domain PF|00155"
                                                                                                                                      /gene="At1g62960; F16P17.11"
39. .1712
                                                                                                                                                                                                                                                                           /organism="Arabidopsis/db_xref="taxon:3702"/chromosome="I"
                                                                            /gene="At1g62960;
/codon_start=1
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                                                                                                                                                                                                                                                   /clone="RAFL04-20-B08"
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REFERENCE
AUTHORS
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VERSION
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F16P17/c
                                                                                                                                                                                                                                                                                  REFERENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 1586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 1349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA 1468
                                                                                                                  Sakano, H., Liu, S.X., Yu, G., Lee, J.M., Lenz, C., Pham, P., Toriumi Chin, C., Chiou, J., Choi, E., Chung, M., Gonzalez, A., Howng, B., Liu, A., Vaysberg, M., Altafi, H., Brooks, G., Shehler, E., Chao, O., Conn, L., Conway, A. B., Hansen, N. F., Johnson-Hopson, C., Khan, S., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southbick, A., Davis, R.W., Ecker, J.R., Federspiel, N.A. and
                                                                                                                                                                                                                                                                          Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 98412)
Theologis, A.
                                                                       The sequence of BAC F16P17
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Sequence of BAC F16P17
complete sequence.
                                               Unpublished
                                                                                                     Theologis, A.
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AC011000.3
                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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NRQRLQSIYTELVEGLKELGIECTRSNGGFYCWADMRGLISSYSEKGEIELWKLLNI
GKINVLPGSCCHCIEPGWFRICESNLSERDVPVVMNRIRKVCETCKSQN"
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DELGNPDGVIQLGLAQNNKLSLDDWVLENPKEAISDGLSISGIASYEPSDGLLELKMA
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KWRTGVDIIHVPCRSADNFNNSMVVLDRAFYQAKKRGVRIRGIIISNPSNPMGSLLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:7109456
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Pred. No. 5.3e-36;
0; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98412
from #
                                                                     from Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 bp DNA linear PLN 13-0
Arabidopsis thaliana chromosome
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                                                                       thaliana chromosome
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                                                                                                                                                                                                                                                    Toriumi, M.,
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On Feb 29, 2000 this sequence version replaced gi:6453846.
The sequence is of BAC F16917 from Arabidopsis thaliana chromosome
1. The sequence does not represent the sequence of the entire
insert of this clone. It is shorter by 10039 bp because we submit
only the unique sequence of the clone. However, in order to
facilitate the joining of overlapping clones in the future, for
creation of larger contigs, we provide small overlaps (200 bp)
between overlapping sumbitted clones. The 5' end of this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (29-SEP-1999) Plant Gene
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/db_xref="GI:8493576"
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QIDSALDSLSDWYFESCGSVSLSGLEHPKLRAFLTQVGLFISRRDFVUGRLDLKYED
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KLYKEMARRIEEERPLVGQCLPLWDBLRSKIKDWYAKFNVYEERQVEKLVERREKKSY
KLYKEMARRIEEERPLVGQCLPLWDBLRSKIKDWYAKFNVYEERQVEKLVERREKKSY
KLYKEMARRIEEERPLVGQCLPLWDBLRSKIKDWYAKFNVYEERQVEKLVERREKKSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/protein_id="AAF75798.l"
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DIITLNTLIDGCCRAKRHLLHGFCQVGNVNVAQDLFQEMISNGVSPDIVTCNTLLAGL
CENGKLEKALEMFKVFGKSKMDLDTATCNIIINGMCKGNKVDEAMDLFNSLTVNGVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(10587.
/gene="F16P17.2"
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MVDSMVSEGCSPDVVTFSTLIKGYCKAGRVDDGLELFSEMCQRGLVADTITYNALIHG
HPAWAAAFILDPLYLIKDSSGKYLPPFKCLSPEQEKDVDKLITRLVSRDEAHIAMMEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                           comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform from Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(1043. .1069,1256.
/gene="F16P17.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1043. .2844)
/gene="F16P17.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Contains weak similarity to T-type calcium channel isoform from Rattus norvegicus gb|AF125161. EST gb|R3003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCKVGDLNGAQDIFEEMVSSGVCPDTITFRSMLAGLCTKAELQKGLTMLEDLQKSVDH
                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Contains multiple PPR Repeats PF|01535.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="F16P17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                               /gene="F16P17.6"
27943. .29520
                                                                                                                                                                                                                                                                                                                                                                                     KSFLDMLS"
27943. .29
                  GNRISDAVALVDQMVEMGYKPDTVTFTTLIHGLFLHNKASEAVALIDRMVQRGCQPDL
VTYGAVVNGLCKRGDTDLALNLLNKMEAAKIEANVVIYSTVIDSLCKYRHEDDALNLF
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KMEILGISHNLYTYNILINCFCRCSRLSALALLGKMKKLGVBDIVTLNSLLNGECH
                                                                                                                                                                                                                                                                                                                                                                                                                                               DCFPNVVTYSTLIKGFCKAKRVEEGMELFREMSORGLVGNTVTYTTLIHGFFQARDCD
NAQMVFKQMVSVGVHPNILTYNILLDGLCKNGKLAKAMVVFEYLQRSTMEPDIYTYNI
MIEGMCKAGKVEDGWELFCNLSLKGVSPNVIAYNTMISGFCRKGSKEEADSLLKKMKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASGDYREILRNRLSDIIKVDDAVDLFGDMYKSRPFPSIVEFNKLLSAVAKMNKFELV
ISLGEØMOTLGISHDLYTYSIFINCFCRRSQLSLALAVLAKMMKLGYEPDIVTLSSLL
NGYCHSKRISDAVALVDQMVEMGYKPDTFTFTTLIHGLFLMKASEAVALVDQMVQRG
COPDLYTYGTTVNGLCKYRGDIDLASLLKKMEKGKIBADVVIVNTIDGLCKYKHMDD
ALNLFTEMDNKGIRPDVFTYSSLISCLCNYGRWSDASRLLSDMIERKINPNVTYFSAL
IDAFVKEGKLVEAEKLYDEMKIRRSIDPDIFTYSSLINGFCMHDRLDEAKHMFELMISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F16P17.5"
25427. .27325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Strong similarity to O-methyltransferase 1 Arabidopsis thaliana gb|U70424 and contains an O-methyltransferase domain PF|00891."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Contains similarity to a 14kDa protein found on ER-derived vesicles from Saccharomyces cerevisiae gi|6331384. ESTs gb|T22150, gb|AI100633, gb|AA395672
                                                                                                                                                                                                                                                                         /note="Contains a RepB PF|01051
multiple PPR PF|01535 repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Contains a RepB PF|01051 protein domain multiple PPR PF|01535 repeats."
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/gene="F10F17.4"

join(24159 . 24411,24497 . 24561,24604 . 24903)

/gene="F16F17.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(22027. .23274)
/note="Contains similarity to Limpet1_transposon."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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INFVVLPESILOGFICVFYLLYGHWFMALLCVPYLYYNFHLYSRKQHLIDVTEIFNLL
                                                                                                                                                                                                                                                      this
                                                                                                                                                                                                                                                                                                                                                                                                                               {	t DGPLPNSGTYNTLIRARLRDGDREASAELIKEMRSCGFAGDASTIGLVTNMLHDGRLD}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVDVGGGIGTIIGQVTSKYPHIKGINFDLASVLAHAPFNKGVEHVSGDMFKEIPKGDA
IFMKWILHDWTDEDCVKILKNYWKSLPEKGKVIIVEVVTPEEPKINDISSNIVFGMDM
{\tt KKGKLVKAEKLYEEMIKRSIDPNIFTYSSLINGFCMLDRLGEAKQMLELMIRKDCLPN}
                                                                                                                                                                                                                                                                                                                 /gene="F16P17.6"
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/gene="F16P17.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMLAVSSGGKERSLSQFETLASDSGFLRCEIICHAFSYSVIELHK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/protein_id="AAF75800.1"
/db_xref="GI:8493577"
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join(18492. .18563,19155. .19336,19434. .19560)
/gene="F16917.3"
                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MQRSISLTAKRLFVHWNLQGIGNPPTVPSFFNLCGSGCWERSFA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MRVFELIGSNEQFAEMFNRTMSEASTLIMKKVLEVYKGFEDVNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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EST gb|AA728420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256;
                                       mRNA, I
U35779
                                                                                    Triticum aestivum 1-aminocyclopropane-1-carboxylate
                  U35779.1
                                                                                                         TAU35779
                                                             partial cds
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4 TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC 63
                                                                                                                                                                                                                                            CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAAGCTCACGACGCTCTCACCTGTCTCATCTCCAACCCAACATTTGCTGATATCCGCA 45001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCGGGGGCCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 45061
TCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATCTG 44723
                                                             TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                                                                       GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 44764
                                                                                                                                                           GGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCCGGT
                                                                                                                                                                                                                                                                                                          ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA 44882
                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTCCAATCCAAAAAATGTTCAGAGATTTGTGAAAACCAACAGGCAGAGATTGCAGAGT 44941
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complement (35247. .35753)
/gene="F16P17.8"
/gene-"F16P17.8"
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/note="Contains weak similarity to leaf protein from Ipomea nil gbp185101 and contains a RepB PF|01051 protein and multiple PPR PF|01535 repeats."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F16P17.7"
32949. .34790
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TYSILLDGLCKYGKLEKALVVFEYLQKSKMEPDIYTYNIMIEGMCKAGKVEDGWDLFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNSLIRCLCNYGRWSDASRLLSDMIERKINPNVVTFSALIDAFVKEGKLVEAEKLYDE
MIKRSIDPDIFTYSSLINGFCMHDRLDEAKHMFELMISKDCFPNVVTYNTLIKGFCKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDDAVDLFGEMVQSRPLPSIVEFNKLLSAIAKMNKFDLVISLGERMQNLRISYDLYSY
NILINGCRESQLPLALAVLGKMMKLGYEBDIVYLSSLLNGYGEGKRISEAVALVDQM
FVMEYQPNYYFNTILHGLFLHNKASEAVALIDRMVARGCQPDLFTYGTVVNGLCXR
DIDLALSLLKKMEKGKIEADVVIYTTIIDALCNYKNVNDALNLFTEMDNKGIRPNVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSLKGVKPNVIIYTTMISGFCRKGLKEEADALFREMKEDGTLPNSGTYNTLIRARLF
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/protein_id="AAF75803.1"
/db_xref="GI:8493580"
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FKQMVSVGVHPNILTYNILLDGLCKNGKLAKAMVVFEYLQRSTMEPDIYTYNIMIEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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Pred. No. 9.5
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1089 bp

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AUTHORS
TITLE
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AUTHORS
TITLE
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  GTTGTCATTGTATTGAACCCGGCT 391
                                                                                        AGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGGTTCTT
                                                                                                                                                        GGCTTCTCTATTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAG
                                                                                                                                                                                                                                                                   ACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGA 247
                                                                                                                                                                                                                                                                                                                 CGGACACGCGCGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAAGAATGT 187
                                                                                                                                                                                                                                                                                                                                                                                                       AGATTGCCAGATTCTCATCTGTGTCGACCCCGACCCCAGCGCCTTCTTGTTGCCCATGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                              AGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCCAGCGCTTGCTCGTCGTTATGCTCT
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                                              AGCGCAGGCTTTGGGACAGGCTGTTGGAGGAGGCGAAGGTCAATGTCACCCCAGGTTCAT 1063
                                                                                                                                      GGGT - - TCTACTGCTGGGCAGACATGAGCAAGTTCATCCGGTCTTACAGCGAGAAAAGGAG
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1 (bases 1 to 1089)
Subramaniam, K., Abbo, S. and Ueng, P.P.
Isolation of two differentially expressed wheat ACC synthase cDNAs and the characterization of one of their genes with root-predominant expression
Plant Mol. Biol. 31 (5), 1009-1020 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Direct Submission
Submitted (11-SEP-1995) Kuppuswamy Subramaniam, USDA-ARS,
Submitted (11-SEP-1995) Kuppuswamy Subramaniam, USDA-ARS,
Beltsville Agricultural Research Center, Plant Molecular Biology
Baltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum.
Triticum aestivum
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL Submitted (01-OCT 1999) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The orientation of the sequence is from T7 to SP6 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October1998 version). The genomic sequence was searched against the non-redundant database NRP(PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNAbank and the CDNA sequence database at RGP. Protein similarities of the cording regions were searched against NRP with BLASTP2.0. ESTs represent the identified CDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGCCATTGCATTGAGCCGGGTT
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Eukaryota; Viridiplantae; Streptophyta; E
Spermatophyta; Magnoliophyta; Liliopsida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only
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                                                                                                                                                                         ACGCHFLPLARHESAPTLSLGSSHCQKEVPCNRTQFSSDPLRAISNANGLADLIISMV FLAARKREPNQEQHGSSNGVPMMALQIDLHNGSSNLTTSPE"

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Similar to receptor protein )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                        kinase,
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DMOSOME 6,
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.4073)

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CSSRMEPDKSCSLTTSDTHARPPHPNHGRRRRGYARRLVHVVLLLRRRGGRGVRGG
DGGGGDGDGEVVRGGFGVVRPRRGVAVRPRRGGGGGAAVVRLRAQLPALSLTU
NRNESIFLIINSEEKAMLFSRKTDVLEMLMVEKAPTALIAKMLAEDLGLGSLRSTVDI
DAHCSKSSHECSNGAEQTIHRPHIPNEGRIPCHQVSANERKHGVRTIGKGTIPKRST
LMKPTASQLARGNEJIFVKNSTQSKKSVGVRSDRSTMSSNDCTYQAAKRQKLERGHLN
LMKPTASQLARGNEJIFVKNSTQSKKSVGVRSDRSTMSSNDCTYQAAKRQKLERGHLN
/note="ESTs AU030008(E50477),AU078239(E50477) correspond to a region of the predicted gene.
                                                                                                                                                                                                                                                                                        STDNFNISITALEIAYNQAKKRGIKVRGVLISNPNNPTGSFVPKQTLHDLLEFAAEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTRHGDSEFQRQQQQQQQQQQDTDVH"
join(24594...24979,25296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(14588. 14693,15191. 15299,15896. 15968. 16609. 16683,16765. 16827,17295. 17364,17675. 17845, 18666. 18766,19737. 19845,2254. 20410,20534. 20683, 21424. 21542,21971. 22225,22674. 23145,23660. 23750)) /note="Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19, hypothetical protein (AL031018)"
                                                                                                                                                                                                                                                IHLISDEVFAGSTYGSGKFVSVAEVVDDLEDFDKGRVHIIYGLSKDLSLAGFRVGVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthase (U35779)"
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PSGRNDHQHASVPHRGIGSNVPVCTANRPRHLDNICKTPDECRDDLFKFKARPVDKKE
FKLSTGRKGKQAPLSELFNKLTLTTEARRALDHRTADLPNYITTKLNIIPYLLAAMAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAIYKINQFQPLVKGSDKPVQGPPKLVVLQMDMAIHTYEDIMRLTENLSEKYIIGYGA
SSTVKCELKSGKAIAVKRLYSQYNHSLREFFFELETIGSIRHRLVSLHGFSLSPHG
NLLFVDYMENGSLMDLLHGPSKKVKLMWDTRLKIAVGAAQGLAYLHHDCNERIIHDV
KSSNIILLDENFEAHLSDFGIAKCVPSAKSHASTYVLGTIGYIDPEYARTSRLNEKSDV
YSFGIVLLELLTGKKAVDNESNLHQLILSKADDNTVMEAVDSEVSVTCTDMGLVRKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30922.
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DSLILNNNLLVGEIPAQLANCFSLNNLAFQEFVIQQFIWTCPDGKELLEIPNGKHLLI
SDCNQYINHKOSFLONPLLHVYCQDSSCGHSHGQRVNISKTAIACIILGFIILLCVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Similar to 1-aminocyclopropane-1-carboxylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA84789.1"
/db_xref="GI:6006359"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDLYRETNHDAGVHSPVQFLLEPVTDSTSFDENQSKTTEFRGSNAGRKHSNEPTKQDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt GNMSKLSYLQLNDNELVGTIPAELGKLEELFELNLANNNLQGPIPANISSCTALNKFN}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPIPSTLSQ1PNLKTLDLAQNQLTGD1PRL1YWNEVLQYLGLRGNSLTGTLSPDMCQL
TGLMYFDVRGNNLTGT1PESIGNCTSFEILDISYNQISGEIPYNIGFLQVATLSLQGN
TRITCKIPDVIGLMQALAVLDLSENELVGPIPSILGNLSYTGKLYLHGNKLTGVIPPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .31079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26934,27845. .28007,28363. .28482,29210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .25323,25853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .26051,26163
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Matches
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Best Local Similarity
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                                                                                                                        CGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTACCAAAA 67
                         AGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGCTCT 127
                                                                                          CCGGGTTTCGGGGTAATATATTCCTATAATGAAAGCATCGTGACAGCAGCTGCTA
250;
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                        VPGNDRKEYVLFRGAROWWYRGEVKKGGVLVAAASRSRESVYYYFSVQRTTGGKRWRA
MSGIT"
                                                                                                                                                                                                                                                                                                                           /translation="MLPAATAAVTVSAIDVGDGEERPLCRNGSSCDGPTATHRPWWPWCQWPSESLSIGSGLAFDVSTGTVCSNAYSNKGQFLDQALFHLFGWAEIPALCWEKKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTVALREIRKYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSHAVLALQEAAEAYLV GLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA" complement(join(49556. .50196,50838. .51051))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA84793.1"
/db_xref="G:6006363"
/db_xref="G:6006363"
/tanslation="Matateevaaaaaaageapppppppavveeakealeapkpeeapk
AEEGBEEKAEGEKEKEKAKKERKPRARKPRSAGPHHPPYFEMIKEAIMALDGNGKAGS
SPYATAKYMGEQHMGYLPANYRKVLAYQLRNFAAKGRLVKVKASFKLSAAEEKKATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted gene.
Similar to histone H3 (AB015760)"
                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAA84796.1"
/db_xref="GI:6006366"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /---.vouvv. .39930,61242. .61397,61635. .61777,62523. .62570)
/note="hypothetical protein"
/codon start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEATMEMRSTTVSEGGARIEMRSTIVTEGNARIEMCRAPLLFCRPPAACHSNPAVPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA84794.1"
/db_xref="GI:6006364"
/translation="MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKKPHRYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(47867. .48205,48314.
/note="EST D15300(C0425) corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAARSKAAKGVVGGAKRKRTPRPSAAAAKKPASSAEAKKAVPPARPARAKRARKAAPA
KPMQPPKSIRSAISKKANKASA"
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/note="ESTs AU078183(C62904),C73912(E21020)
a region of the predicted gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA84792.1"
/db_xref="G116006362"
/taanslatton="MUDDNAIRERDHALAEKKAAIAERDMAFTORDAAMAERNAAVV
ERDNALAALELALMPNKRHARMGGRKMSGGAFTKLLSRLAAEGHDLSTPVDLKDHWAK
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/db_xref="GI:6006361"
/translation="MSVTLHTNLGDIKCEVFCDQAPRTAENFLALCASGYYDGTIFHR
NIKGFMIQGGDPTGTGKGGTSIWGKKFADEFRESLKHNARGVMSMANSGPNTNGSQFF
                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similar to water stress inducible protein (U74296)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join (39025.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAA84795.1"
/db_xref="GI:6006365"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Similar to Arabidopsis thaliana chromosome II BAC
T32F12, hypothetical protein (AC005314)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITYAKQPHLNGHYTVFAKVIHGFEVLDLMÈKAQTGPGDRPLAEIRLNRVTIHANPLAN
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5
                                                                                                                                                                                                                  .98;
                                                                                                                                                                                         0;
                                                                                                                                                                                      Score 144.2; DB 8
Pred. No. 1.4e-34;
0; Mismatches 138
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                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                 Length 143113;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCTTCTCTATTGGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATTTGTTTGTTG-ATGCTTTGGATCAAGTGGGGATTGAGTGCTACAAGAGCAGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGGAAACTCAAAAGAATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGT--TCTACTGCTGGGCAGACATGAGCAAGTTCATCAGGTCTTACAGCGAGAAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana 1-aminocyclopropane-1-carboxylate ACS12 (At5g51690) mRNA, complete cds. AF336920 AF336920.1 GI:12484204 FLLCUNA.
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Yamada, K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Yamada, K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Toriumi,M., Yu,G., Brooks,S., Chao,Q., Ghen,H., Karlin Neumann,G., Kim,C., Lam,B., Miranda,M., Nguyen,M., Chen,H., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1488)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etgu, P., Yamada, K., Liu, S.X., Sakano, H., Brooks, S., Chao, Q., Chen, H., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Rarlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (17-Jan-2001) Plant Gene Street, Albany, CA 94710, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theologis, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34908
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Dβ δÃ Ър δÃ В QУ В 204 Дb Qy DЬ Qy

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BASE COUNT
ORIGIN
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Best Local Similarity
Matches 243; Conserv
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               CTTGTTGTCATTGAATTGAACCCGGCTACTTTAGCCTCTG 404
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                                                                                                                                                                                          AGCATATTCGGTTTGTGG-AAGGTTTGAAACAATTAGGAATACCATGTGCTGAGAGTGGT 1251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTTCTTATGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCTGGTTTTAGAGCTGGAGTCATCTACTCCTTTCATGAAGACGTAGTAAATGCTGCAA 1072
CAGCCTGTTATTGTATAGAACCAGGTTGGTTCAGGTGCTG 1409
                                                                                 GAGAACTCGAGTTATTTGAGAAGCTATTGACTGTTGCTAAGATTAATGCCACTCCAGGAA 1369
                                                                                                                                                                      GGTGGGT--TGTATTGTTGGGTAGACATGAGCAGTTTACTGACATCTTACAGTGAGAAAG
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KFRTGVELIPVHCRSSDNFTVTVSALEQALNQARKRGSKVSGILFSNPSNPVGNILSR
ETLCDILRFAQEKNIHVISDEIFAGSVYGDKEFVSMAEIAGSGEFDKTRVHIIYGLSK
DLSIPGFRAGVIYSFHEDVVNNAKKLMEFSSVPVLVQRILISLLSDVRFIEGYMAAHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRIRDKHIRFVEGLKOLGIPCAESGGLYCWUDWSSLITSYSEKGELELFEKLLTVAK
INATPOTACYCLEPGWFFCCFTALADEDIPVIMERIRQLAESFRS"
289 c 359 g 454 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 127.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 1.6e-29;
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                                                                                                                                                                           1309
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MEDLINE REFERENCE AUTHORS DEFINITION ACCESSION RESULT 9 AB010074/c COMMENT REFERENCE SOURCE KEYWORDS VERSION Locus TITLE AUTHORS ORGANISM JOURNAL JOURNAL Submitted (07-JAN-1998) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934) On Sep 15, 2000 this sequence version replaced gi:2760170. Address for correspondence: Kaos@kazusa.or.jp For the latest information on annotation of this clone close 86212 Arabidopsis thaliana genomic AB010074 BA000015 Structural analysis of Arabidopsis thaliana chromosome 5. Sequence features of the regions of 1,456,315 bp covered nineteen physically assigned P1 and TAC clones DNA Res. 5 (1), 41-54 (1998) Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 98290546 and Tabata, S. Sato, S., Arabidopsis thaliana (strain:Columbia) DNA, AB010074 BA000015 AB010074.2 GI:10177866 Nakamura,Y. (sites) (bases 1 to Kaneko, T., Kotani, H., 86212) DNA, Nakamura,Y., chromosome DNA Embryophyta; Tracheophyta; clone_lib:Mitsui Asamizu, E., Miyajima, N. P1 clone:MIO24 covered by PLN 27-DEC-2000 P1

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FEATURES
                                              CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MIO24
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, oak Ridge National Laboratory,
http://compbio.ornl.gov/grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zcol.iastate.edu/gl-bin/sp.cgi).
Genes encoding trRNas are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K10D11 and the 3' clone is MJM18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGIIOLGLAESTRWASENLMESMMQSDDGEFDISSIAMYKPFEGLLELRVAFADFMSR
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REFAQEKNIHVISDEIFAGSVYGDKEFVSMAEIAGSGEFDKTRVHIIYGLSKDLSIPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTPQTLGELIMMSRRRSYMRRAVEMRKQNPYTVRLSNIFSHSLPKPYAP" complement(join(2918. .3767,3876. .4036,4292. .440 4519. .4860))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAGVIYSFHEDVVNAAKKLMRFSSVPVLVQRILISLLSDVRFIEGYMAAHRQRIRDKH
IRFVEGLKQLGIPCAESGGGLYCWVDMSSLLTSYSEKGELELFEKLLTVAKINATPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACYCIEPGWFRCCFTALADEDIPVIMERIRQLAESFRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GASSLVGASFLEKLFPRLLPSEKVKAAVSEDVQVSTHPLHEEVKLTTETDNMSIGFPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVPVPVKQVTSVPFDWEETPGQPYPCFVDTSPPELLDQPLPPPPMYGDVETSSDIFDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1494.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="MIO24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
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13. .8741,8843. .8
.9538,9772. .9825,
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.8887,8984. .9061,
5,9931. .10027,10121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4405,
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CDS

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CDS

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AMPLPYTNHLOWYSSKINSVYQHKSOEEEGNNNRILTYYQTAFHGLAAQLTQEEAERL
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GISTARMFDRYLLEKEPSEUDSPEGSDGASFNSSVADQQAEIETVAKVTHEKGKRNDTQ
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EINVERNSTSCLGQPVIVGYLLAGSIGPGLKFISEMVVCETVAQFGVVFLLFA
LGLEFSMTKLKVVGPVAVLGGLOIVLLMFLGCVVGLLFALLPVLGGNSGLLQGIISMGKL
LLILSTYLTVASLLTMSFVPRFLKLMIQLSSQTNELKQLAAVAFCLLSAWCSNIGLS
LLILSTYLTVASLLTMSFVPRFLKLMIQLSSQTNELKQLAAVAFCLLSAWCSNIGLS
                                                                                                                                                                                                                                                                                                                                                                                                    GKKRSKLLAQANVMEEALMIYREVQAGRTGVEGFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLLNHFKSDAEVATVIGHEVGHAVARHVAEGITKNLWFAILQLVLYQFVMPDLVNTMS
ALFLRLPFSRKMEIEADYIGLLLLASAGYDPRVAPTVYEKLGKLGGDALGDYLSTHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains similarity to peptidase
gene_id:MIO24.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
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VRPVIONSASSEDLKISDQGEEPAHKKAKTDTNTCKKESSRRVSSKESDVYKKETLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKEDQVLDDQWIQKSRKKDSKAHAATSHLEGISWEVLVVNEPIVNAFCLPAGKIVVFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDDIKDKFTKFSYRSLFGLVIFGKFGEKGQVWIIRFDMIQTGLVQRHDYQPVENDVLI
PSLDLYYRSGLRTDACISDS"
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YLLLLGTTALSLYTTPLLFKLIPSAMNLGYLLRWFPSENSSPNEVILFSRSIYI"
join(13548. .13771,14028. .14130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVNYEVSGGPFIKKPCQRLLARQKIPLCMALSVLARSTSNSDQPQALNLSESEAYNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLPTYSFKNLTKTAEVGERALFIPKQGGRYDCGTIFVKGYDSSLGENDLARALLEHFS
PCGMISRIYFQTNDAGEAVLKHYFIVMLQGTEDALKLNGSDMGGCNLEVHDATERDEF
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                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                        /note="gene_id:MI024.12"
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17217. .17560)
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/translation="MAIIASTFGTGLSYAGELPFKPVTGGEVGKKQQRMVVVRAEGGG
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/protein_id="BAB11240.1"
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.16860,16938. .17116,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATCTGATGTAAGATTCATTGAGGGATACATGGCAGCACAGGCAAAGGATCCGGGATA
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                                                                                                                                                                                              synthase.
X96947
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                                                                                           Musa
                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
                                                                                                                                                                       X96947.1 GI:1255948
                                                                                                                       Musa
                                                                                                                                           1-aminocyclopropane-1-carboxylate
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SRGPNFLSLEILKPDLLAPGVNILAAWTGDMAPSSLSSDPRRVENILSGTSMSCPHV
SGVAALIKSRHEDWSPALIKSALMTTAYVHDNMKFNFLDASGAAPSSPYDHGAGAILDF
LRATDPGLYVDJGPQEYFEFLCTQDLSPSQLKVFTKHSNRTCKHTLAKNPGNLNYPAI
SALFENNTHVKAMTLRRTVTNVGPHISSYKVSVSPFKGASVTVQPKTLNFTSKHQKLS
VENDEDETETENTHVKAMTLRRTVTNVGPHISSYKVSVSPFKGASVTVQPKTLNFTSKHQKLS
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RNRDRTDMEVYSSFDVPLRKQARRSEIGGLPADIGGFLAPPAASSCQKSEAPVWKGEE
TEDEPLYGIVSVMGRSRKMEDSVTVKPNLCKPEVNRQRPVHFFAVYDGHGGSQVSTLC
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join(30819. 31283,31350. 31694,31761. .3
/note-"gene_id:MIO24.11"
/codon_start=1
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RARIEAAGGRVLVVDGARVEGILATSRAIGDRYLKPMVAWEPEVTFMRRESGDECLVL
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/protein_id="BAB11245.1"
/db_xref="GI:10177875"
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Pred. No. 2.8e-29;
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                                                                            GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
CTGCTCTCCGACAAGGAGTTCACCAGAAACTACATTGCGGAGAACCAGAAGAGGATCAAG 1138
                                                            GCTACCAAGATGTCGAGCTTTGGACTCGTCTCCTCCCAGACTCAGTACCTCCTCTCGGTT
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University of Singapore, Lower I
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                                                                                                                                                                                       Conservative
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/number=1
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589 .>1372
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22. .109
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GLDASKALADFMGELEGNKVKFEPHKLVLTAGSTSAVGTLMFCLAEVEGEAFLLPTPY
YPGFDRDLKRRTGAEIYPIHCGSPHOERVFKAALEKAYQGTLMFCLAEVEGVLVTUNSON
PLGTTMTRCELDTLMTFVVAKDIHLISDEICSGTSFDAPGFVSVMEAIEGRQHVSHRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="1-aminocyclopropane-1-carboxylate synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110. .241
/gene="bacs2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKIVYQVGLNISPGSSCHSHEPGWFRVCFANM"
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/gene="bacs2"
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/db_xref="taxon:4641"
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Submitted (18-APR-1997) J. Liu, Department of Botany, National University of Singapore, Lower Kent Ridge Road, Singapore 1192
REPUBLIC OF SINGAPORE
On Apr 19, 1997 this sequence version replaced gi:1255946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Musa acuminata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (27-MAR-1996) J. Liu, Department of Botany, National University of Singapore, Lower Kent Ridge Road, Singapore 119260, REPUBLIC OF SINGAPORE
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                                                                                                                 /codon_start=1
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/protein_id="CaAA55647.1"
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/db_xref="GI:1945275"
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                                                                            SSCHCDEPGWFSVCFANM"
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/number=1
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/gene="bacs1"
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/db_xref="taxon:4641"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Malus x domestica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosida; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                               Submitted (12-OCT-2000) NRSL, University Building, College Park, MD 20742, USA
                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                    2 (bases 1 to 1400)
Trivedi, P.K. and Solomos,
                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                              partial cDNA
                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1400)
Trivedi, P.K. and Solomos, T.
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/note="authority: <1. .1385
                                            /tissue_type="fruit"
/dev_stage="ripening"
                                                                                           /organism="Malus x domestica"
/cultivar="Granny Smith"
/db_xref="taxon:3750"
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Pred. No. 3.8e-25;
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                                                                                                                                                                                                                                                                                                                         Dong, J.G., Kim, W.T., and Yang, S.F. Cloning of a cDNA enc
Direct Submission
Submitted (09-NOV-1993)
of California at Davis,
                                                                                                                                  2 (bases 1 to 1618)
Dong, J.G.
                                                                                                                                                                                                                             Cloning of a cDNA encoding synthase and expression of planta 185, 38-45 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicoty; Georgia; eurosida; Rossidae; eurosida; Rossaceae; Malusideae; Malus
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/product="AcC Synthase"
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Dong, Vegetable Crops,
b, Davis, CA 95616-8631,
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Malus x domestica
                                                                           1-aminocyclopropane-1-carboxilic
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                                                                                                                               Malus domestica acc synthase AJ011518
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34; Conservative
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//Protein_id="AAA03472.1"
//Bb_xref="GI:417972"
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/product="1-aminocyclopropane-1-carboxylate
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/clone_lib="Library
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/clone="pAAS2"
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                                                                                             GGCCTTCCGGGTTTTCGAGTTGGCGCCATCTACTCCAACGACGACATGGTTGTGGCCGCC 1205
                                           GCTACAAAAATGTCAAGCTTTGGTCTTGTTTCTTCTAAACTCAGCACCTTCTCTCCGCC 1265
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Studi di Milano, Via Celoria, 26 - 20133 Milano-IT,
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Direct Submission
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VLIFPYYPREDLKWRTGVEIVPHICTSSNGFQITFTALEEAYQBAEKRNLEVKGV
LVTNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSETISVMEVLKDR
NCDENSEVMJRYHVYVSIJKDLGLEGFEVGAIYSNDDMYVAAARKMSSFGLVSSQTQH
LLSAMLSDKXLTKNYLAENHKRLKQRQKKLYSGLQKSGISCLNGNAGLFCWVDMRHLL
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/number=3
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/protein_id="CAA09670.1"
/db_xref="GI:3790175"
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join(<1. .4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="acc synthase"
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57.9%;
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Rosaceae; Maloideae; Malus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-JUN-1998) Akihiro Itai, Faculty of Agriculture, Tottori University, Laboratory of Horticultural Science; Koyama-cho Minami 4-101, Tottori, Tottori 680-8553, Japan (E-mail:itai@pear.agr.tottori-u.ac.jp, Tel:81-857-31-6749,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Itai,A., Tomomitsu
Direct Submission
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99168766
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Pyrus pyrifolia (strain:Ninomiya) ripening fruit cDNA to mRNA
Pyrus pyrifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax:81-857-31-6749)
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                                                                                                          /Codon_start=1
/product="1-aminocyclopropane-1-carboxylic acid synthase"
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/protein_id="BaA76389,1"
/db_xref="GI:4586426"
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LAENQLCFDLLESWILAKNPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMYDEMAET
ROMKYTFDUNLTVLTAGATSANETFIFCLADPGEAFLLFTPYYPGFDRDLKWRTGYEI
ROMKYTFDUNLTVLTAGATSANETFIFCLADFGEAFLLFTPYYPGFTMTRNELYLLLS
FVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRCDENEWORVYHVYSLSKDLG
FVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRTGCENEWORVHVYVSLSKDLG
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87. .15
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SPGSSCHCTEPGWFRVCFANLPERTLDLAMQRLKAFVGEYYNVPEVNGRSQSSHLSHS
RGQSLTKWVSRLSFDDRCPIHGR"
                                                                KQRQKNLVSGLQKAGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNI
                                                                                                LPGFRVGAIYSNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRL
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/strain="Ninomiya"
/db_xref="taxon:3767"
/tissno +---- "
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l. .1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="fruit"
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l. .1778
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Search completed: March 11, 2003, 01:20:16 Job time: 1686 secs
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                                                                                           1092 CAACGTCAGAAAAATCTCGTCTCCGGCCTT-CAGAAAGCTGGCATTAGCTGCCTCAATGG 1150
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Result
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE RESULT 1 BM437295 COMMENT DEFINITION JOURNAL TITLE ORGANISM Department of Biochemistry University of Nevada MS200, Reno, NW 89557-0014, UTel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu 1 (bases 1 to 664)
1 (cramer,G.R. and Cushman,J.C. Vitis vinifera. Vitis vinifera Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eu BM437295

WVA017C10_54085 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera cDNA clone VVA017C10 5, mRNA sequence.

BM437295

BM437295.1 GI:18459017 FORWARD: T3 20mer BACKWARD: T7 21me Unpublished (2002) Contact: Cushman JC An expressed sequence tag datal Vitis vinifera var. Chardonnay PCR PRimers Vitaceae; Vitis. USA for abiotic stressed eudicots; EST 31-JAN-2002 Tracheophyta; leaves of

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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., I Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., I Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., 1
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119 c 152 g 197 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available through: ResGen, Invitrogen Corp. South Memorial parkway Huntsville, AL 35801 For further in call: (800) -533-4363 or contact via email: ccu@resgen.com Insert Length: 1667 Std Error: 0.00 High quality sequence stop: 422.
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Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoemaker.
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/clone_lib="Gm-c1069"
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/db_xref="taxon:3847"
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0; Mismatches 125;
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                                                   GAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT
                                                                                                   TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
CTTGTTGTCATTGTATTGAACCCGGCTACTTTAG
                                                                                                                         TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGC 244
                                                                                                                                                                                                                                                                                                                                                  AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 124
                                 GAGAGCTTGAGCTGTGGGAGAAGCTCTTGAATGTAGCTAAGATAAACGTGACTCCAGGGT
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                                                                                                                                                                                                                                                                                                                 AAAAGTTGACAAGATTTTGTGCCGCTTCAGCACCAACACAGAGCCTATTAGTTGCAATGC 475
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BQ118313
BQ118313.1 GI:20170275
EST.
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Restrepo, S., Griffiths, H., van der Hoeven, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
Contact: Robin Buell
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Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cdna@resgen.com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation of a set of potato cDNA clones for microarray analyses
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EST603889 mixed potato tissues
3' end, mRNA sequence.
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XhoI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
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/tissue_type="mixed tissues"
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/clone="cmmmx^"
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
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                 which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesix Kit (catalog number 200401) was used to synthesix Kit (catalog number 200401) was used to synthesix the cDNA. First-stranded synthesis was performed with 5-methyl dCTP, hence the liqated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V-A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGAGAGAGTCTCGAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhOI site within the first-strand synthesis primer was then restricted by digestion with XhOI; all XhOI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into
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Stratagene's pBluescript(tm) II XR Predigested vector
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seedlings"
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/clone_lib="Gm-c1027"
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BQ764374
BQ764374.1
                                                                                                                                                                                    1 (bases 1 to 654)

Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)

Contact: Waugh R, Marshall DF
                                                                                                    Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotlan
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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/organism="Hordeum vulgare"
/cultivar="Optic"
/db_xref="taxon:4513"
                                                                   Location/Qualifiers
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0; Mismatches 122
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyaddi, Tsukuba, Ibaraki 305-0074
Tel: 81-298-36-4359
                                                                                                                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 685)
                                                                                                                                                                                                                                                                                            mRNA sequence.
AV782646
AV782646.1 GI:19801436
                                                                              Large scale analysis of Arabidopsis full-length Unpublished (2002)
                                                                                                                                                Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
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AV782646 RAFL4
                                                                                                                 and Shinozaki, K.
                                                                                                                               Arakawa, T., Shibata, K., Shinagawa, A.,
                                                                  Contact: Motoaki Seki
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143 c 184 g 158 t 1 others
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/clone_lib="anther, yellow
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/lab_host="DH10B"
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Pred. No. 1.7e-39;
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                                                                                                                                                                                                                                                                                                                                                               mRNA
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                                                                                                                                  Muramatsu, M.,
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                                                                                                                                  Hayashizaki,Y.
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REFERENCE
AUTHORS
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BM953903/c
                                                                                                                                                                                            SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGTTGTCACTGTATCGAACCAGGATGGTTCCGTATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGAGATTGAGCTGTGGAACAAGCTCTTGAACATTGGCAAGATCAATGTCATACCAGGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCCGGGGGCTTAGATCCGCTGCTATCTACTCGTTCAACGAGAGTGTTTTATCCGCTTCA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTACACGGAGCTCGTGG-AGGGGTTGAAAGAGTTAGGGATCGAGTGCACAAGAAGCAA
                                                                                                                                                                                                                                BM953903.1
EST.
l (bases 1 to 550)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phas
                                                                                                                                                                                                                                                                                 BM953903 550 bp mRNA linear EST 14-MA sam67f01.y1 Gm-c1069 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1069-4489 5', similar to TR:Q9SNN8 Q9SNN8 SIMILAR TO 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.;, mRNA sequence.
                                                                                                                                                                                        soybean.
Glycine max
                                                                                                       Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for
                                                                                                                                                                                                                                                                           BM953903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RAFL04-20-B08"
/clone_lib="RAFL4"
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/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="rosette plants"
/lab_host="SOLR"
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                                          Beck, C.
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                                                                                                                                                         AGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGG
                                                                                                                                                                                                                                                                                                                                                                      CAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTAT 122
GTCAGCCTGCCATTGCATAGAACCAGGATGGTTTAGGATTTG
                                 TTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG
                                                                                                                                      GTGCTGG--TATGTACTGTTGGGCTGATATGAGTGGATTAATCCGACCTTATAGTGAGAA
                                                                                                                                                                                                                                                                           GCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAG
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                                                                                                                                                                                                           AGTGCACGATGAATTTGTGG-GTTGTTTAAGTAAACTAGGAATCAAGTGTGCCAAGAGCA
                                                                                                                                                                                                                                              AATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCA 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available through: Re
South Memorial Parkway Huntsville,
call: (800)-533-4363 or contact: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Shoemaker R/Public Soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Public Soybean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Location/Qualifiers
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ritter, E., Kohn, S., Shin, T
Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from degenerating cotyledons of 9-10 day old etiolated seedlings for the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker.
a 135 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Degenerating
etiolated seedling"
/lab_host="DH10B"
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/clone_lib="Gm-c1069"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ibrary was constructed in the laboratory
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63.4%;
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Pred. No. 1.5e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ResGen, Invitrogen Corp.
e, AL 35801 For further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jackson, Y., Cardenas, M., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14;
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Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BJ447315.1 GI:21125948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Hordeum vulgare subsp. vulgare"
/cultivar="Akashinriki"
/db_xref.="taxon:112509"
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GTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTAT 258
                                                         TTTGTGCAAAAATTTATTGAGGTTAACAGGTTGAGGCTGCGGAAAATGTATAATACATTT 120
                                                                                      TTCACTCAAAAGTTCATCGAGGTAAACAGAGGGAAACTCAAAAGAATGTACGCTGCATTC 198
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410 bp mRNA linear EST 04-DEC-2001 so37b07.yl Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1039-110 5' similar to TR:Q43201 Q43201
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shoemaker R/Public Soybean EST Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y, Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Public Soybean EST Project
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: /note="vector: pBluescriptII SK+; Site_1: EcoRI; Site_2: XhOI, This cDNA library was constructed from mRNA isolated from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Ogden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhOI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhOI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhOI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHOB host cells (Gibco BRL). This
                                                                                                                                                                                                                                                                                                                                                                                                                     library was constructed by Dr. Randy Shoemaker." 72 c 110 g 130 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="whole seedling without cotyledons"
/lab_host="DH108"
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/clone_lib="Gm-c1039"
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/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      singleton, see http://cgpdb.ucdavis.edu/ for
Plate: QGC23 row: F column: 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Church,S., Jackson,L. and Bradford,K. Lettuce and Sunflower ESTs from the Compositae Genome Project
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QGC23F17.yg.ab1 QG_ABCDI
QGC23F17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kozik,A.,
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H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
H., Van Damme,M.S., Livingston,K., Zhou,Y., Lai,Z.,
tolkman,J., Lai,Z., Lai,Z., Lai,Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-(530)-742-1742
1-(530)-752-9659
                                                                                                                                 /note="Vector: pBRcDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TRG_LIB-QG_ABCDI lettuce salinas
                                                                                TAG_TISSUE=flowers post-fertilized
TAG_SEQ-TGCCATCGGG"
70 c 181 g 245 t
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/lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                                                                                         /organism="Lactuca sativa"
/cultivar="Salinas"
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                   Score 136.8; DB 14; Pred. No. 1.7e-35;
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172
            /note="Site_1:
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TGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
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                                                                                                                                                                                                                                             Email: msekiertc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Na
Akiyama,K., Enju,A., Oono,Y., Sakural,T., Carninci,P., K.
Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A.,
,M., Hayashizaki,Y. and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA
Unpublished (2002)
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/clone_lib="RAFL16"
/lab_host="DH10B"
                                                                                       /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAAGCTGATGAGATTTTCATCAGTGCCAGTTCTAGTTCAAAGGATACTTATCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                                                                                                                                                                             Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
NC, 27695-8008
                                                                                                                                                                                                                                                                                               Whetten, R.W., Kinlaw, C.S., Retzel, E. The Pine Gene Discovery Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 515)
                                                                                                                                                                                                                                                                                                                                                                                                                  AW064832 515 bp mRNA linear ST36D01 Pine TriplEx shoot tip library Pinus taeda ST36D01, mRNA sequence.
AW064832 AW064832.1 GI:6019904
                                                                                                                                                                                                                                                                                                                                                                                           loblolly pine.
                                                                                                                                                                          primer:
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                                                                                                                                                                                                      919-515-7800
919-515-7801
                                                                                                                                                                        rosswhet@unity.ncsu.edu
imer: 5' lambda TriplEx2 Sequencing
/clone_lib="Pine TriplEx shoot tip library"
/lab_host="E. coll BM25.8"
/note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1
sfir (A); Site_2: Sfir (B); Shoot tips (approx. 2 cm fro
apex) were collected during the spring, frozen and used
for mRNA isolation. The SMART-PCR method (Clontech) was
used to prepare a library from 1 ug total RNA, using the
Lambda TriplEx vector. Plasmid subclones in pTriplEx wer
                                                                                                       /organism="Pinus taeda"
/db_xref="taxon:3352"
/clone="ST36D01"
                                                                                                                                                             Location/Qualifiers
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Pred. No. 2.3e-32;
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Pinus; Pinus.
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TGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGGG--TCTTTATTGTTGGGTTGAAATGGGAAGCTTGATGCCATCTTATAGTGAGAANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGAGCTTAATCTTTGGGATAAATTATTGAATGAAGCANAAATAANTGTCACTCCAGGGA 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Egukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW040322
EST283186 tomato mixed elicitor, clone cLET513, mRNA sequence.
AW040322
AW040322.1 GI:5899076
                                                                                                                                                                                                                                Clemson University Genomics Institute
                                                                                                                                                                                                                                                                           Generation of ESTs from tomato leaf tissue Unpublished (1999)
Contact: CUGI
                                                                                                                                                                                                                                                                                                                                                                  D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tomato
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                                                                                                                                                                                        http://www.genome.clemson.edu/orders/index.html
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/cultivar="Rio Grande PtoR
/db_xref="taxon:4081"
/clone="cLET513"
/clone_lib="tomato mixed e
/tissue_type="leaf"
                                                                                                                                                                         sequence
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1e-29;
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BTI Lycopersicon esculentum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGGCCCTTATAATGAAAAGGGAGAGCTTGAGCTGTGGGAGAAGCTCTTGAATGTAGCT
                                                                                    Email: msekiertc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sall. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index e.html) for forther
                                                                                                                                                                                                                                                                                        Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shihagawa,A., Muramatsu,M., Hayashizaki,Y.
                                                                                                                                                                                                                                                Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 423)
                                                                      details
                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                    and Shinozaki, K.
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                                                                                                                                                                                                                                                                                                                                                                                                            scale analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 bp mRNA line RAFL9 Arabidopsis thaliana cDNA clone
1. .423
/organism="Arabidopsis
                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF/"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; CLET - Inoculated with a variety of disease responselicitors. Plants exposed to 2,6 dichloroisonicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. site was destroyed during cloning."

68 c 126 g 154 t
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Pred. No. 4.1e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201;
             Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
                                                                                                                                               Large scale analysis of Arabidopsis full Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
                                                                                                                                                                                                                                                              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV820681 AFL11 Arabidopsis thaliana
                                                                                                              Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 420)
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dehydration (1, 2, 5,
hr) treatments"
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/clone="RAFL09-55-E15"
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modified pBluescript vector. Please visit our
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Pred. No. 2.
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                                                                                                                                                 Ibaraki 305-0074,
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10, 24 h
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Search completed: March 11, 2003, 01:40:14 Job time : 1217 secs
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Best Local Similarity 70.7
Matches 171; Conservative
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                                                                                                                                                       343
                                                                                                                                                                                      223 CATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTATTGTTGGGCCGACATGAGCGGATTG 282
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                                                                                                                                                                                                                                                                                                                              163 AACAGAGCGAAAACTCAAAAGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGG 222
                                                           TG 404
                                                                                                                       site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="plants at various developmental stages from germination to mature seeds"
/lab_host="pH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to various treatments (dehydration, cold, high salt, ABA, heat and UV). Dark-grown plants"
). Dark-grown plants"
105 c 64 g 129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAFL11-11-109"
/clone_lib="RAFL11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      26.5%;
                                                                                                                                                                                                                                                                                                                                                                        Score 107.2; DB 10; Length 420; Pred. No. 2e-25; 0; Mismatches 68; Indels 3;
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Maximum Match
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Query
Match Length !
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compu
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-724-194-3
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US-08-378-313-18
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US-08-673-768-1
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 Sequence
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TCA	CGA - TGA	TTT	GTACGCTGC	ACAC	TGAC	GGGGTTC AGGTTTC		3.4 14.5 3.2 11.9 3.2 11.9 3.2 11.9 3.2 11.9 3.4 7.4 3.8 7.4 3.8 7.4 3.8 7.4 3.8 7.4 3.8 7.4 3.8 7.1 3.6 6.8 3.6 6.8 3.6 6.8 3.6 6.8 3.6 6.8 3.6 6.8 3.6 6.8 3.6 6.8 3.7 1 3.8 7.1 3.8
TTG	GCT/	CTA:	ATTO	CAA	GAG	CAG	larity Conserva:	11.5 1 11.9 9 11.9 9 17.8 46 7.8 46 7.4 5 7.4 5 7.2 7 7.1 15 7.1 15 7.1 15 6.8 1 6.8 1 6.8 1 6.8 1 7.1 15 7.1 15 7.1 15 7.1 15 7.1 15 7.1 15 7.1 15 7.1 15 7.1 15 7.1 15 7.2 7 7.2 7 7.2 7 7.2 7 7.3 87 6.8 1 6.8
CTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG	CTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCCGGTT 	TICTCTATIGTIGGGCCGACATGAGCGGAITGATICGATCCTACAGCGAAAAAG 	TGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGG 	TCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 	AAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC 	TTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACTGCCA	E 2 4	1098 3 1497 2 7587 4 9060 4 46819 4 46819 1 1473 3 5931 4 24417 2 7218 1 610 4 15393 4 11962 4 289 4 1962 4 289 4 1962 4 289 4 197 Sept Sign Of Sept NUMBER: 10-C
GAA	GAC GAT	TGG	AC-	ACT ATG	TCA	GGT GGT	8.2 1.2	997 887 999 999 999 999 999 999 110 110 110 110
000	AAGI NGGI	GCAC	aggg H	CAA	TCT/	GCC1	90 90	98 3 97 4 99 4 111 3 111 3 111 3 113 4 17 2 19 4 10 4 10 4 10 4 10 4 10 4 10 4 10 7 10
GCT	TGT	GACA GACT	TTTG	AAGT	ATTT	ATCI	Score Pred. 0; Mis	
CTI	TAA! TGA!	TGAC	AAG/ AAG(TCA:	CAG CCG	ACTO ACTO		09-043-627 -08-860-577 -08-378-313 -08-378-313 -09-453-702 -08-783-774 -09-134-001 -08-783-774 -09-32-463 -09-453-702 -09-453-702 -09-453-702 -09-443-702 -09-244-796 -09-244-796 -01_ETHYLEN -771,482A -797,17644, -9ublishe
ΨAG	CAT	GGG - TGG	AAC	CGA	CCC	CTTA	194. No.	-043-6 -860-3 -378-3 -378-3 -378-3 -378-3 -378-3 -378-3 -378-3 -378-3 -7583-7 -5846-7 -791-1
COL	TGC: AGG:	ATTO	TGG	GGT	GAC ATC	TAA		6, NT 8 92 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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	CTCC	AGCGAA AGTGAG	GGAAAGCAGC AAAGAGCAAT	TCA/	TCAGCTCCGACGCAGCGCTTGCTCGTCGTTATGC	CTAC	Length 1743 Indels 3	
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SEQ ID NO 2
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APPLICANT:
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CURRENT FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yip, Win Kin
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Transiently Activated Stress-Inducible Plant Promoters
FILE REFERENCE: 02370-097000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (3103)..(4066)
NAME/KEY: CDS
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LOCATION: (3007)..(3102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: 1-aminocyclopropane-1-carboxylic acid (ACC) OTHER INFORMATION: synthase (ACS) LE-ACS7 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Lycopersicon esculentum
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                               361 GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAG
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Local Similarity 56.3%;
es 224; Conservativo
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                                                                                               AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC
                                                                                                                                CAATGCTGGGT--TGTTTTGTTGGGTGGATATGAGACATCTTTAAGTTCAAACACATTT
                                                                GATGGAGAAATGGAATTATGGAAGAAAATAGTGTACGAAGTAGGGCTAAATATTTCAGCT
                                                                                                                                                                 AAACGACATGAAATGCTAGTTGGTGGTCTTAAACAAA-TTGGAATAAGGTGCCTTGAGAG
                                                                                                                                                                                                                     AGAATGTACGCTGCATTCGTGGGGGGGTTGAAGAACTCGGCATCCGATGCACGGAAAG
GGATCGTCATGCCATTGTACAGAACCGGGTTGGTTTCG
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Shiu, Oi Yin
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Pred. No. 1.2e-24;
0; Mismatches 171; Indels 3
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Patent No. 5998702
GENERAL INFORMATI
                                                                                                                                                                                                     Query Match
Best Local Similarity 55.9
' ~~~ 226; Conservative
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
                              1090
                                                                                          1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reynolds, John F
TITLE OF INVENTION: Transger
TITLE OF INVENTION: Synthase
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 180 N.
STREET: 4700
CITY: Chicago
                                                                                                                                                     970
                                                           121
181
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1384 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                   61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                         LOCATION:
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                                                ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGGAAACTCAAA 180
                                                                                                                                                   GGTCTTCCCGGGTTTTCGAGGTTGGGACCATTTACTCGTACAACGATAATGTTGTGAGGACA 1029
AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
                              ATGTTGTCGGATGAAGAGTTTACGGAGAAGTACATAAGGATAAACCGTGAAAGGCTTAGG 1149
                                                                                          INFORMATION:
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180 N. Stetson, 2 Prudential Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruttencutter, Glen E.
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55.9%;
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Pred. No. 9.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08846826A Patent No. 6194639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              TELEX: 831-494
INFORMATION FOR SEQ ID NO:
                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 961 base pairs
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                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 879
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL ACC NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                               TELEPHONE: 215-567-2991
                                                                                                                                 NAME/KEY:
                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Nadel Esq., Alan S. REGISTRATION NUMBER: 27,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/846,826A FILING DATE: 01-MAY-1997
                                                                    LOCATION:
                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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103..194
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SYSTEM: PC-DOS/MS-DOS
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55.9%;
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Pred.
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86.6;
No. 8.
DB 4;
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             Length 961;
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                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: 01-MAY 1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9
FILING DATE: 01-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nadel Esq., Alan S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                  INFORMATION FOR SEQ ID NO:
                              SEQUENCE CHARACTERISTICS:
LENGTH: 968 base pairs
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                TELEPHONE: 215-965-1280
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
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                                                                                                                                                    REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-11
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS:
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US-08-846-826A-1

NAME/KEY: LOCATION:

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MOLECULE TYPE: FEATURE:

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                    APPLICANT: Reynolds, John F.
TITLE OF INVENTION: Transgenic Plai
TITLE OF INVENTION: Synthase Genes
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
            FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
                                                                                                                                                             COMPUTER READABLE FORM:
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STREET: 4700
CITY: Chicago
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NAME: Mueller, Lisa REGISTRATION NUMBER:
                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                      ADDRESSEE:
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Ruttencutter, Glen E.
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                                                                                                                                                  Floppy disk
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                                                                                                                                                                                                                                                                                                                                  Transgenic Plants
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                                                                         US/08/860,577
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Pred. No. 4.3e-20;
0; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                  Expressing
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                                                                                                                                                                                                                                                                                                             Sequence 3, Applica Patent No. 5824875
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                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                  APPLICANT: RANU, RAJ
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: STELECOMMUNICATION INFORMATION TELEPHONE: 312-616-5400
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPETWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
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                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SANTANGELO LAW OFFICES
STREET: 315 WEST OAK STREET, STE 7
                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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ZIP: 80521
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US-09-043-627-7
; Sequence 7, Application US/09043627
; Patent No. 6124525
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Best Local :
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APPLICANT: Botella,
TITLE OF INVENTION:
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                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
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CLASSIFICATION:
                APPLICATION NUMBER: US/0 FILING DATE: 20-MAR-1998
                                                                                                                                                       COUNTRY: USA
ZIP: 08540-3662
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Pred. No. 1.
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1.4e-19;
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US-09-043-627-9; Sequence 9, A
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                                                                                                      Sequence 9, Application US/09043627 Patent No. 6124525 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                         CORRESPONDENCE ADDRESS:
                                                                          APPLICANT: Botella, TITLE OF INVENTION:
                                                                                                                                                                                                                      1045
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LENGTH: 1096 base pairs
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APPLICATION NUMBER:
FILING DATE: 20-SEP-
                                                             NUMBER OF SEQUENCES:
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           STREET:
                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT
                                                                                                                                                                                                                                                                                    GATGCCGAAATGAAGCTATGGGGCACGATTTTGAACGATGTGAAACTTAACGTTTCACCA 1044
                                                                                                                                                                                                                                         GGTTCTTGTTGTCATTGTATTGAACCCCGGCTACTTTAGCCTCTG
                                                                                                                                                                                                                      GGCTCTTCCTTTCATTGCCAGGAGCCTGGTTGGTTCAGAGTCTG
                                                                                                                                                                                                                                                                                                       AAAGGAGACTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC
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                                                                                                                                                                                                                                                                                                                                                                             AAAAGGTACCATATTTTCACAAAGAGACTTG-AGAAAGTGGGGATTAACTGCTTGAAGGG
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Princeton
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                            MATHEWS,
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                                                                          Jose Ramon
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53.2%;
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                            COLLINS, SHEPHERD & GOULD P.A.
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Pred. No. 1.4e-18;
0; Mismatches 186;
             Suite
                                                                          SYNTHASE
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 35
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bernstein, Scott N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: AU PN559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: USA COUNTRY: USA 7TP: 08540-3662
1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 215; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
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GGTTCTTCCTTTCATTGCGCTAATCCAGGATGGTTTCGGGTTTG 1094
                                                                                                                                                                     AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGGATGCACGGAAAG 240
                                                                                                                                                                                                                                                                                                                                                                                GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
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                              GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                   GAAGCAGAGATAGAACTGTGGAAAGTGATAATCAACGAAGTTAAATTAAATGTTTCTCCG
                                                                                                     AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC 360
                                                                                                                                                                                                                                                                            ATGTTATCAGATGAATTTGTGGATAGGTTCATTACTGAGAGTGCTAAAAAGGCTTGCA 873
                                                                                                                                        CAATGCGGG--GCTATTTTCTGGATGGATTTGCATCATCTCCTCAAGGAGCAAACTGAT
                                                                                                                                                                                                         AAAAGGCACAGAGCCTTC-ACATGGGGGCTATCTCAAGTAGGCATTGGTTGTTTGAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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GENERAL INFORMATION:
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BIRD, COL
APPLICANT: FLETCHER,
TITLE OF INVENTION: 1
1162
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MOLECULE TYPE:
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LENGTH: 1712 base pairs
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                                 301
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                                                                                                                                                                                                                                                                   925 GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTCGCTTCC 984
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TELEPHONE: 822-0944
                                                                                                                                                                                                                                                                                                61 GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: CUSHMAN DARBY AND CUSHMAN STREET: 1100 NEW YORK AVENUE N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
GAGGCGGACGTCCGGCTGTGGCGGGGTGATCATCAACGACGTGAAGCTCAACATCTCGCCG
                                                                                                                                  GGGCGGCGCAGGGTCTTTACGG-ACGGCCTCAAGCGAGTCGGGATTCATTGCTTGGACGG 1103
                                                                                                                                                                                                                     ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGGAAACTCAAA 180
                               AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
                                                                  AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAACTCGGCATCCGATGCACGGAAAG 240
                                                                                                                                                                                                    ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 1044
                                                                                                                                                                                                                                                                                                                                                                                                   214;
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53.0%;
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Pred. No. 6.5e-18;
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                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        ORGANISM: MUSA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
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APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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TELEPHONE: 822-0944
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                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 16,773 REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                CLONE:
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AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAACTCGGCATCCGGATGCACGGAAAG
                                                                                                                                ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                ATGTTGGGAGACGAGGAGTTCACCACGAGTTTCTTAGCGACGAGCCGGACGAGGTTGTGC 104
                                                                                                               GCGAGGAAGATGTCGAGCTTTGGACTGGTCTCGTCGCAGACGCAGCTCCTGCTTCC 984
                                                                                                                                                                             GGCGTCCCTGGCTTCCGCGTCGGCGTCATATACTCCTACAACGACGCCGTGGTCAGCTGC 924
                                                                                                                                                                                                         GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
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                                                                                                                                                                                                                                                        Score 78.8; DB 4;
Pred. No. 6.5e-18;
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US-09-043-627-1
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                                               Matches
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                                                                                                                                                                                                                                              TELEFAX: 609-924-3036 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PNI
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PNI
FILING DATE: 02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
                                                                                                                                               FEATURE:
                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 609-924-8555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                              Local
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                                                                                                                                                                                                                                                                                                                      NAME: Bernstein, Sco
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                      NAME:
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1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTACTACAACGAGAACGTGCTCACTACT 60
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                                               208;
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                                                             Similarity
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SYSTEM: PC-DOS/MS-DOS
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                                                          .2e-17;
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RESULT 13
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                                                    Matches
                                                                                    Query Match
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                                                                                                                                                                                                                                         TELEPHONE: (970) 224-3100 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RANU, RAJIND
TITLE OF INVENTION: ONE
TITLE OF INVENTION: SYN
TITLE OF INVENTION: IN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                  Local Similarity
nes 217; Conserv
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/724,194 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SANTANGELO LAW OFFICES STREET: 315 WEST OAK STREET, STE
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
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N: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
N: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
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53.7%;
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                                                                    Score 72.4; DB 1;
Pred. No. 1.3e-15;
                                                     Mismatches 181;
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US-08-695-412B-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STILES, JOHN I.
APPLICANT: MOISYADI, STEFAN
APPLICANT: NEUPANE, KABI R.
TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
TITLE OF INVENTION: DUA SEQUENCES AND PROCESSES FOR CONTROLLING
TITLE OF INVENTION: RIPENING OF COFFEE
NUMBER OF SEQUENCES: 13
                                                                                                                                                      REGISTRATION NUMBER: 34,831
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/485,107
FILLING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1212 GAGGCGGAGATGGTGCTGGAAGGTGATTATTAATGAGGTGAAGCTAAACGTGTCTCCG 1271
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                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WordPerfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    978
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                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0:
FILING DATE: 12-AUG-1996
   TOPOLOGY: 1
)LECULE TYPE:
                                                       TYPE:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                     STRANDEDNESS: single
                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                            NAME: GRIFFITH, CALVIN P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: JONES,
                                                                      CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACGCGGG--GCTCTACTTCTGGATGGATTTGCGGAAGCTTCTAGAAGAAGAAGACGTTT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCTATCCGACGACGTTTTCGTGGAGCGGTTCCTCGCGG---AGAGCCGGAGCTTGGGG 1094
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                                                                                                                          (216)
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                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                     linear
                                                                                                                                        (216) 586-7050
     cDNA to
                                                                                                                          579-0212
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RESULT 15
US-09-255-154D-11
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          APPLICATION NUMBER: US/08/695,412
FILING DATE: 12-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRIFFITH, CALVIN P.
                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,154D
FILING DATE: 22-Feb-1999
CLASSIFICATION: 435
                                                                                                                                                                                                                              ZIP: 44114
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: JONES, DAY, REAVIS & POGUE
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
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                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS v. 5.1 SOFTWARE: WordPerfect v. 6.1
                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                     STATE: OHIO
                                                                                                                                                                                                                                                                                                                   CITY: CLEVELAND
                                                                                                                                                                                                                                                                                                                                       STREET:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                    OF INVENTION: PURIFIED PROTEINS, RECOMBINA DNA SEQUENCES AND PROCESSES
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178..1653
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NEUPANE, K
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                                                                                                                                                                                                                                                                                     USA
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Pred. No. 1.
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Search completed: March 11, Job time: 48 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 17.9%;
Best Local Similarity 52.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 265036600002 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                      GGCTTATCTTTCCATTGCTCAGAACCAGGATGGTTCAGAGTTTG 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTTCCCTGGATTCAGAGTTGGCATTTTGTATTCATATAATGACGCTGTTGTCAGCTGT 1086
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                                                                                                         GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG
                                                                                                                                                GAGGCAGAAATGGAACTTTGGAGGATCATAATACATGAAGTCAAGCTCAATGTTTCACCA 1383
                                                                                                                                                                                                                        CAGTGCGGGC--CTTTATTTCTGGATGGACTTAAGGAGACTCCTCAGGGAGTCCACATTT 1323
                                                                                                                                                                                                                                                            GCAAGGCATGGTCTTTTCACAAGAGGACTTG-CTCAAGTAGGCATTGGCACCTTAAAAAG
                                                                                                                                                                                                                                                                                                                                    AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG 240
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                                                                                                                                                                                                                                                                                                                                                                                                            ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTAGAAAAATGTCGAGTTTCGGCCTTGTTTCAACACAAACTCAGCATCTGATTGCATCA 1146
                                                                                                                                                                          AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (216) 579-0212
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LOCATION: 178.
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Pred. No. 1.3e-15;
0; Mismatches 191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191; Indels
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Run
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
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length: 0
length: 2000000000
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404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gggttgccggggttcaggat.....cccggctactttagcctctg 404
                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                       Maximum Match
: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
0: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
1: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compu
                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/US07_
/cgn2_6/ptodata/2/pubpna/PCT_N
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4423.601 Million cell updates/sec
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                                                                                                                                                                                                                                                   _NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

O	C							ဂ	c	C	G		O			O		Result No
19	17	16	15	14	13	12	11	10	9	8	7	σ	υ	4	ω	2	1	ult No.
29.8	29.8	29.8	29.8	29.8	29.8	29.8	30	30.2	30.2	30.2	30.2	30.4	31.6	53.6	107.6	107.6	194.8	Score
7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.5	7.5	7.5	7.8	13.3	26.6	26.6	48.2	Query Match
13819	1113	398	398	398	398	398	353	17239	7960	2302	2302	1416	46819	1488	1344	748	1743	Length
10	9	10	10	9	9	9	10	10	10	12	10	9	9	9	9	10	10	DB
US-09-738-626-1 US-09-764-877-2596	US-09-738-626-3191	US-09-880-107-1211	US-09-962-436-152	US-09-954-531-508	US-09-954-531-291	US-09-954-531-90	US-09-924-035A-68	US-09-764-869-2326	US-09-764-869-2327	US-10-033-528-1711	US-09-920-300A-1711	US-09-938-842A-583	US-10-114-170-72	US-09-938-842A-1726	US-09-938-842A-1571	US-09-770-149-16	US-09-776-529A-1	ID
Sequence 1, Appli Sequence 2596, Ap	Sequence 3191, Ap	Sequence 1211, Ap	Sequence 152, App	508,	291	Sequence 90, Appl	Sequence 68, Appl	Sequence 2326, Ap	Sequence 2327, Ap	Sequence 1711, Ap	⊣	Sequence 583, App	Sequence 72, Appl	Sequence 1726, Ap	Sequence 1571, Ap	Sequence 16, Appl	Sequence 1, Appli	Description

ALIGNMENTS

US-09-776-529A-1

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                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1743
TYPE: DNA
ORGANISM: Rosa kerdinal
                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 285; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tagawa Greenhouses, Inc.
APPLICANT: Ranu, Rajinder S.
TITLE OF INVENTION: A 1-Aminocyclopropane-1-Carboxylate Synthase Gene From Rosa to
TITLE OF INVENTION: Ethylene Levels In Roses
FILE REFERENCE: Tagawa-Rose
CURRENT ETLING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: US 08/724,194
PRIOR APPLICATION NUMBER: US 08/724,194
PRIOR FILING DATE: 1996-10-01
PRIOR FILING DATE: 1996-10-19
PRIOR APPLICATION NUMBER: US 08/711,482
PRIOR APPLICATION NUMBER: US 08/717644
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-09-30
                                                                            1292
                                                                                                                                                       1352
                                      125
                                                                                                                  65
                   TCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAA 184
                                                                                                 TTTCAGACACCAAATTTATGCATAAGTTCATCGAGATTAACAGAGAAAAGGCTCCGTGGAA 1411
                                                                              AAAAGTTGACAAGGTTCTCTTCTATCTCCGCCCCATCCCAACGGTTGCTTATCTCTATGC 1351
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                         48.2%;
71.2%;
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                                                                                                                                                                                                                                        Score 194.8; DB 10; Length 1743; Pred. No. 2.5e-57; O; Mismatches 112; Indels 3;
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20
Qγ
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; LCCATION: (1)...(748)
; OTHER INFORMATION: n = A,T,C or
US-09-770-149-16
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US-09-770-149-16/c
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SEQ ID NO 16
LENGTH: 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                                61
                                                                                                                                                                                      Local Similarity
                                                                                                                   1 GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                               GCGAGAAGGATGTCGAGCTTCACGCTTGTCTCGTCTCAGACACAACATATGCTGGCTTCT 498
                                                         GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTTCTT
                                                                                              GGTCTTCCTGGTTTCCGCGTGGGAACTATATACTCGTACAACGATAATGTTGTTCGGACA
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                                                                                                                                                                      232;
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Allen, Keith
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Slader, Ted
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Woessner, Jeffrey P.
Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09770149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raines, Tracy M.
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                                                                                                                                                                      Conservative
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                                                                                                                                                                                    26.6%;
57.4%;
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                                                                                                                                                                                    Score 107.6; DB 10; Pred. No. 3.1e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1571
LENGTH: 1344
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Harper, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1571, Application Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS,
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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                                                      1101
                                                                                                                          1042
301 AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC
                                                                                                                                                            181
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                                                                                    GCCAAAAAGTTGACGAGATTTTCATCCATTTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                                                                                                                                                                                                                                                                                                      GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
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                                                                                                                      AGACGGTACGATACCATTGTGGAAGGGCTT-AAGAAGGCAGGGATTGAGTGTTTGAAAGG
                                                                                                                                                           AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
                                                                                                                                                                                             ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                                                                                                                                                                                                GCGAGAAGGATGTCGAGCTTCACGCTTGTCTCGTCTCAGACACAACATATGCTGGCTTCT
                                                                                                                                                                                                                                                                                                                                    GGTCTTCCTGGTTTCCGCGTGGGAACTATATACTCGTACAACGATAATGTTGTTCGGACA 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATCTTCGTGCCACTGCTCGGAGGTCGGATGGTTTAGGGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACGCAGG--GCTATTTTGTTGGATGAATTTGGGTTTCTTGCTCGAAAAGAAAACTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         26.6%;
57.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107.6; DB 9; Pred. No. 4.2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1344;
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us-10-114-170-72/c
                                                                                                                   RESULT 5
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APPLICANT: Zhu, Tong
APPLICAYS: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PL
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-938-842A-1726
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                           Sequence 72, Application US/10114170 Publication No. US20030023075A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1726
LENGTH: 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1726, Application Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Harper, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                              361
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hes 192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
           APPLICANT:
                                                                                                                                                                              GGCGGTTCGTTCCATTGCCATGAACCGGGATGGTTTAGAGTATG
                                                                                                                                                                                                                                                                                                                                                                                           AGAATGTACGCTGCATTCGTGGCGGGGGTTGAAGAACTCGGCATCCGATGCACGGAAAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTCTGCCTGGTTTAAGAGTTGGTATAGTATACTCTTACAATGACAGGGTGGTTCAGATC 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTTGCCGGGGTTCAGGATGGGCGTTATCTACTCCTACAACGAGAACGTGCTCACTACT 60
                                                                                                                                                                                                                     GGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCCTCTG 404
                                                                                                                                                                                                                                                                GATTCGGAAACCGAACTATGGCGTGTGATTGTTCACCAAGTGAAGCTCAACGTGTCTCCA 1203
                                                                                                                                                                                                                                                                                                         AAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGTAAACGTTACTCCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAAGGAAAATGTCGAGTTTCGGTCTTGTTTCGTCACAAACGCAGCATTTGATCGCTAAA 966
                                                                                                                                                                                                                                                                                                                                                    GCCAAAGCCGGTTTGTTGTTGTGGATGGATTTAAGAAATCTTTTGAAGACAGCACGTTT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTTATCCGATGAAGAGTTTGTAGACGAGTTTATCCGCGAGAGCAAATTGCGGTTAGCT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGCTCTCGGACACGCGGTTCACTCAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAAAAAGTTGACGAGATTTTCATCCATTTCAGCTCCGACGCAGCGCTTGCTCGTCGTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGATCTTCGTGCCACTGCTCGGAGGTCGGATGGTTTAGGGTTTG 1262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
      Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/09938842A
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Pred. No. 2.5e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLANTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1488;
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                                                                                                 GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
             APPLICANT: Wang, xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37493 CATCGTGGCGGTGCAGGTAATTTCGCTGAAGATCGACAAAAAGCTTCTGACGCTGGTCGT 37434
                                                                                                                                                                                                                                                                                                    37373 GGGAAAAAAGGTGGTCAGAATAGCCATGGT 37344
                                                                                                                                                                                                                                                                                                                                                                                        37433 AAAGGCGGCCAACATAGTGGCGGTAATTTTAAAAACGATCCACAAAGAGCATCAGAAGCA 37374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 CGTGGCGGGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAAGCTTCTCTA 257
                                                                                                                                                                                                                                                                                                                                                318 ATGGGACAAGTTGCTAAACATTGCTAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No._US20030023075A1el Sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGTTGGGCCGACATGAGCGGATTGATTCGATCCTACAGCGAAAAAGGAGGAGCTCGAGCT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1 South Pinckney Street CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 46819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.8%;
50.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251-9166
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Pred. No. 6.4;
0; Mismatches
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US-09-920-300A-1711/c
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                                   US-10-033-528-1711/c

: Sequence 1711, Application

: Patent No. US20020131971A1
                                                                                                                                                    B
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                                                                                             RESULT 8
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 583
LENGTH: 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 210121.547

CURRENT APPLICATION NUMBER: US/09/920,300A

CURRENT FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1711

LENGTH: 2302
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Best Local Similarity 57.3%;
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1711, Application US/09920300A Patent No. US20020136728A1
                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: King,
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                               2069
                                                                                                                                                                                                                                                                                                   2129 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCCATGTGCCTTCAAGCCT
                                                                                                                                                      2009 GAGGCTGGCTGGAGAATGA 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 CGGTTCTTGTTGTCATTGTATTGAACCCGGCTACTT 395
                                                                                                                                                                                                                                                                                                                                        145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 AAAAAACCGTTCTCATGCTTGCGGACCAGCTGATTAACAGAGTCGAGTTTATGCATACTAG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 AAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAGGTAAACGTTACTCC 359
                                                                                                                                                                                         265
                                                                                                                                                                                                                                                                                                                                                                  7.5%;
Local Similarity 51.1%;
les 71; Conservation
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King, Gordon E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon E.
                                                          US/10033528
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Pred. No. 2.8;
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US-09-764-869-2327/c

: Sequence 2327, Application US/09764869

: Patent No. US20020061521A1
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RESULT 10
US-09-764-869-2326/c
; Sequence 2326, Application
; Patent No. US20020061521A1
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Matches
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NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2327
LENGTH: 7960
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LENGTH: 2302
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
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CURRENT FILING DATE: 2001-01-17
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC007
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                7660 GAGGCTGGCTGGAGAATGA 7642
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Pred. No. 7.
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US/09764869

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LOCATION: (1)...(353)
OTHER INFORMATION: n = A,T,C
US-09-924-035A-68
US-09-954-531-90; Sequence 90, Apr
                                       RESULT 12
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LENGTH: 17239
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PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 2011US
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
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                                                                                                                                                                                                      288 ATCCTACAGCGAAAAAGGAGAGCTCGAGCTATGGGACAAGTTGCTAAACATTGCTAAAGGT 347
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                                                                                                                           AAACGTTACTCCCGGTTCTTGTTGTCATTGTATTGAACCCGGCTACTTTAGCC 400
                                                                                                                                                                ATCAGACAAAGCAAAACAAAAGGACAAGTAATAGAAGGAGCTGAAATCCTAAGGTTAGTG 194
                                                                                        AAATTTTATTACCGGTTTCTTTCGTATCTGAAATGAAAANNNTCAACTTGTCC 247
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Application US/09954531
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53.1%;
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Pred. No. 1.9;
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Pred. No. 12;
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Query Match
Best Local Similarity
Whiches 61; Conserve
                                                                                                           ; ORGANISM: HOMO US-09-954-531-291
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US-09-954-531-291
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                                                                                                                                                                                               SEQ ID NO 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 291,
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Best Local
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                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR ETLING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/60/233,133 PRIOR FILING DATE: 2000-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77
                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/60/234,009 PRIOR FILING DATE: 2000-09-20
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PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
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CURRENT FILING DATE: 2002-05-02
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NUMBER OF SEQ ID NOS: 1392
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PRIOR APPLICATION NUMBER: US/60/234,567
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PRIOR FILING DATE: 2000-09-18
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                                                                                                                                                      TYPE: DNA
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                      Conservative
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54.0%;
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US-09-962-436-152
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US-09-954-531-508
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CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
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                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 152 LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Soppet, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 152, Application US/09962436 Patent No. US20020081301A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Weaver,
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TYPE: DNA
ORGANISM: Homo sapiens
-09-962-436-152
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PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
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                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using SignatuTITLE OF INVENTION: Sets FILE REFERENCE: 689290-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
                                                                                                                                     PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 568
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Best Local Similarity 54.0
Matches 61; Conservative
                                                                    181 CAAAATAATAACAAATACCACAGAGAGCCCTACATGAGAAAGCCATGTGCCTTCAAGCCT 240
                                                                                    145 CAAAAGTTCATCGAGGTAAACAGAGCGAAACTCAAAAGAATGTACGCTGCATTCGTGGCG 204
241 GGGGATGAGGACTCTAGTTCTCAAATTCTTAGAACATAGCACATGATTCTCCA 293
                               205 GGGGTTGAAGAAACTCGGCATCCGATGCACGGAAAGCAGCGGAGGCTTCTCTA 257
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Pred. No. 2
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Search completed: March 11, 2003, 01:41:27 Job time: 71 secs